```
OM protein - nucleic search, using frame_plus_p2n.model

Run on:         March 14, 2006, 07:44:42 ; Search time 15376 Seconds
                                           (without alignments)
                                           4898.385 Million cell updates/sec

Title:          US-09-976-858-42
Perfect score:  6787
Sequence:       1 MLPVYQEVKPNPLQDANLCS..........MVTNTSNGQPSTLTIFETAL 1325

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters:     11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US09976858_@CGN_1_1_4939_@runat_13032006_170059_11745 -NCPU=6 -ICPU=3
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      GenEmbl:*
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                15:  gb_pl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6787	100.0	4004	8	AY207008	AY207008 Homo sapi
2	6779	99.9	4231	6	AR589389	AR589389 Sequence
3	6779	99.9	4231	6	AX210645	AX210645 Sequence
4	6779	99.9	4231	6	AX686744	AX686744 Sequence
5	6779	99.9	4231	8	AF071202	AF071202 Homo sapi
6	6779	99.9	5832	6	CQ896291	CQ896291 Sequence
7	6779	99.9	5871	6	CS038316	CS038316 Sequence
8	6770	99.7	4515	6	CQ488793	CQ488793 Sequence
9	6770	99.7	4515	6	CQ490536	CQ490536 Sequence
10	6770	99.7	4515	6	CQ492310	CQ492310 Sequence
11	6770	99.7	4515	6	CQ492702	CQ492702 Sequence
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14	6766	99.7	5759	8	AY081219	AY081219 Homo sapi
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22	6760	99.6	6082	6	AR657116	AR657116 Sequence
23	6760	99.6	6082	6	AX141045	AX141045 Sequence
24	6760	99.6	6082	6	AX200905	AX200905 Sequence
25	6760	99.6	6082	6	AX267561	AX267561 Sequence
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27	6600.5	97.3	6140	6	AR367289	AR367289 Sequence
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33	6600.5	97.3	6140	6	AR657117	AR657117 Sequence
34	6600.5	97.3	6140	6	AX141046	AX141046 Sequence
35	6600.5	97.3	6140	6	AX200906	AX200906 Sequence
36	6600.5	97.3	6140	6	AX267562	AX267562 Sequence
37	6510.5	95.9	3863	8	AF541977	AF541977 Homo sapi
38	6003	88.4	4526	9	AY533524	AY533524 Rattus no
39	5988	88.2	4021	9	AF534126	AF534126 Rattus no
40	5765.5	84.9	4415	9	AY533525	AY533525 Rattus no
41	5591	82.4	3372	6	CQ725032	CQ725032 Sequence
42	5391.5	79.4	4878	5	AJ719382	AJ719382 Gallus ga
43	4676	68.9	2940	8	AF071203	AF071203 Homo sapi
44	4330.5	63.8	2890	8	BC041560	BC041560 Homo sapi
45	4232	62.4	4299	8	HSM807262	BX647118 Homo sapi

ALIGNMENTS

```
RESULT 1
AY207008
LOCUS       AY207008                4004 bp    mRNA    linear   PRI 01-JUN-2003
DEFINITION  Homo sapiens ATP-binding cassette transporter C4 (ABCC4) mRNA,
            complete cds.
ACCESSION   AY207008
VERSION     AY207008.1  GI:31322320
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 4004)
  AUTHORS   Kato,R. and Ishikawa,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-2002) Department of Biomolecular Engineering,
            Graduate School of Bioscience and Biotechnology, Tokyo Institute of
            Technology, 4259 Nagatsuda-cho, Midori-ku, Yokohama-shi, Kanagawa
            226-8501, Japan
FEATURES             Location/Qualifiers
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                    ESAKVIQPIFLGKIINYFENYDPMDSVALNTAYAYATVLTFCTLILAILHHLYFYHVQ
                    CAGMRLRVAMCHMIYRKALRLSNMAMGKTTTGQIVNLLSNDVNKFDQVTVFLHFLWAG
                    PLQAIAVTALLWMEIGISCLAGMAVLIILLPLQSCFGKLFSSLRSKTATFTDARIRTM
                    NEVITGIRIIKMYAWEKSFSNLITNLRKKEISKILRSSCLRGMNLASFFSASKIIVFV
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                    NKMFESILKAPVLFFDRNPIGRILNRFSKDIGHLDDLLPLTFLDFIQTLLQVVGVVSV
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ORIGIN

Alignment Scores:
Pred. No.:              0           Length:         4004
Score:                  6787.00     Matches:        1325
Percent Similarity:     100.0%      Conservative:   0
Best Local Similarity:  100.0%      Mismatches:     0
Query Match:            100.0%      Indels:         0
DB:                     8           Gaps:           0

US-09-976-858-42 (1-1325) x AY207008 (1-4004)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
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Db          6 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 65

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
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Db         66 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 125

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
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Db        126 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 185

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Db        186 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 245

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
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Db        246 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 305

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
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Db        306 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 365

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
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Db        366 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 425

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
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Db        426 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 485

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
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Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Db       1026 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1085

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
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Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
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Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
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Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Db       1686 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1745

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
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Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
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Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
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Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
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Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
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Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
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Db       2286 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2345

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Db       2346 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2405

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Db       2406 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2465

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Db       2526 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2585

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2586 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2645

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2646 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2705

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Db       2706 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2765

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
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Db       2766 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2825

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2826 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2885

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2886 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 2945

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2946 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3005

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
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Db       3006 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3065

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
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Db       3066 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3125

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
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Db       3126 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3185

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
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Db       3186 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3245

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
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Db       3306 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3365

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
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Db       3426 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3485

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
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Db       3486 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3545

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3546 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3605

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
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Db       3606 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3665

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3666 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3725

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
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Db       3726 AGCGACAAGATAATGGTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3785

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3786 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3845

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3846 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 3905

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
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Db       3906 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 3965

Qy       1321 PheGluThrAlaLeu 1325
              |||||||||||||||
Db       3966 TTCGAGACAGCACTG 3980

RESULT 2
AR589389
LOCUS       AR589389                4231 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 1 from patent US 6803184.
ACCESSION   AR589389
VERSION     AR589389.1  GI:56636669
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4231)
  AUTHORS   Kruh,G. and Lee,K.
  TITLE     MPR-related ABC transporter encoding nucleic acids and methods of
            use thereof
  JOURNAL   Patent: US 6803184-A 1 12-OCT-2004;
            Fox Chase Cancer Center; Philadelphia, PA
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              0               Length:         4231
Score:                  6779.00         Matches:        1323
Percent Similarity:     99.9%           Conservative:   1
Best Local Similarity:  99.8%           Mismatches:     1
Query Match:            99.9%           Indels:         0
DB:                     6               Gaps:           0

US-09-976-858-42 (1-1325) x AR589389 (1-4231)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              |||||||||||||||||||||||||||||||||||||||||||||||||:::||||||||
Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
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Db        476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db        596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Db        776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Db       1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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Db       1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555
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Qy    481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
Db   1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615
Qy    501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
Db   1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675
Qy    521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Qy    541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
Db   1736 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1795
Qy    561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
Db   1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855
Qy    581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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Qy    601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
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Qy    621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Db   2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095
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Qy    721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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Qy    741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
Db   2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395
Qy    761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
Db   2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455
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Qy    801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Qy    821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
Db   2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635
Qy    841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
Db   2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695
Qy    861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
Db   2696 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2755
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Db   2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815
Qy    901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Db   2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935
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Qy   1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
Db   3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175
Qy   1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
Db   3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235
Qy   1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
Db   3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295
Qy   1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
Db   3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355
Qy   1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
Db   3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415
Qy   1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
Db   3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475
Qy   1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
Db   3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535
Qy   1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
Db   3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595
Qy   1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
Db   3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655
Qy   1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
Db   3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715
Qy   1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy      1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy      1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
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Db      3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy      1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
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Db      3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy      1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
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Db      3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy      1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
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Db      4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy      1321 PheGluThrAlaLeu 1325
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Db      4076 TTCGAGACAGCACTG 4090

RESULT 3
AX210645
LOCUS       AX210645                 4231 bp    DNA     linear   PAT 31-AUG-2001
DEFINITION  Sequence 287 from Patent WO0157058.
ACCESSION   AX210645
VERSION     AX210645.1  GI:15424905
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Rosenthal,A., Hinzmann,B., Schaefer,R., Zuber,J., Tchernitsa,O.,
            Grips,M., Hellriegel,M., Schmitz,A.C. and Sers,C.
  TITLE     Detection of differential gene expression
  JOURNAL   Patent: WO 0157058-A 287 09-AUG-2001;
            Metagen Gesellschaft fuer Genomforschung mbH (DE)
FEATURES             Location/Qualifiers
     source          1..4231
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              0              Length:        4231
Score:                  6779.00        Matches:       1323
Percent Similarity:     99.9%          Conservative:  1
Best Local Similarity:  99.8%          Mismatches:    1
Query Match:            99.9%          Indels:        0
DB:                     6              Gaps:          0

US-09-976-858-42 (1-1325) x AX210645 (1-4231)

Qy         1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db       116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy        21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy        41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy        61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy        81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy       101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy       121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy       141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
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Db       536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy       161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db       596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy       181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy       201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy       221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Db       776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy       241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy       261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Db       896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy       281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy       301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy       321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy       341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Db      1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy       361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Db      1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy       381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Db      1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy       401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375
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Qy      421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy      441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy      461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
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Db     1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy      481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615

Qy      501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy      521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Db     1676 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1735

Qy      541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
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Db     1736 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1795

Qy      561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Db     1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855

Qy      581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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Db     1856 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915

Qy      601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
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Db     1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy      621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Db     1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy      641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
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Db     2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095

Qy      661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
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Db     2096 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2155

Qy      681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
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Db     2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy      701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Db     2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy      721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy      741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy      761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
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Db     2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455

Qy      781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Db     2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2515

Qy      801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Db     2516 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575

Qy      821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Db     2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy      841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Db     2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695

Qy      861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
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Qy      881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
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Db     2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815

Qy      901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Qy      921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
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Db     2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy      941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy      961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
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Db     2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy      981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
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Db     3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy     1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
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Db     3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy     1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
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Qy     1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
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Db     3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy     1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Db     3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy     1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
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Db     3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy     1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
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Db     3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535

Qy     1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Db       3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
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Db       3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
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Db       3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
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Db       4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy       1321 PheGluThrAlaLeu 1325
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Db       4076 TTCGAGACAGCACTG 4090

RESULT 4
AX686744
LOCUS       AX686744                4231 bp    DNA     linear   PAT 29-MAR-2003
DEFINITION  Sequence 3 from Patent WO02079238.
ACCESSION   AX686744
VERSION     AX686744.1  GI:29372313
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Eulenberg,K., Broenner,G., Ciossek,T., Haeder,T. and Steuernagel,A.
  TITLE     Protein disulfide isomerase and ABC transporter homologous proteins
            involved in the regulation of energy homeostasis
  JOURNAL   Patent: WO 02079238-A 3 10-OCT-2002;
            DeveloGen Aktiengesellschaft fuer Entwicklungsbiologische Forschung
            (DE)
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
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US-09-976-858-42 (1-1325) x AX686744 (1-4231)

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Qy          801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Db       3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

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Db       4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy       1321 PheGluThrAlaLeu 1325
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Db       4076 TTCGAGACAGCACTG 4090
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RESULT 5
AF071202
LOCUS       AF071202                4231 bp    mRNA    linear   PRI 21-JUL-1998
DEFINITION  Homo sapiens ABC transporter MOAT-B (MOAT-B) mRNA, complete cds.
ACCESSION   AF071202
VERSION     AF071202.1  GI:3335172
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 4231)
  AUTHORS   Lee,K., Belinsky,M.G., Bell,D.W., Testa,J.R. and Kruh,G.D.
  TITLE     Isolation of MOAT-B, a widely expressed multidrug
            resistance-associated protein/canalicular multispecific organic
            anion transporter-related transporter
  JOURNAL   Cancer Res. 58 (13), 2741-2747 (1998)
   PUBMED   9661885
REFERENCE   2  (bases 1 to 4231)
  AUTHORS   Lee,K., Belinsky,M.G., Bell,D.W., Testa,J.R. and Kruh,G.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUN-1998) Medical Oncology, Fox Chase Cancer Center,
            7701 Burholme Ave., Philadelphia, PA 19111, USA
FEATURES             Location/Qualifiers
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ORIGIN
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Score:                     6779.00        Matches:        1323
Percent Similarity:        99.9%          Conservative:   1
Best Local Similarity:     99.8%          Mismatches:     1
Query Match:               99.9%          Indels:         0
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US-09-976-858-42 (1-1325) x AF071202 (1-4231)

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Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
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Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
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Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
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Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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Db        836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
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Db       3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
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Db       3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
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Db       3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
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Db       3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
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Db       3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
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Db       3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
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Db       4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy       1321 PheGluThrAlaLeu 1325
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Db       4076 TTCGAGACAGCACTG 4090
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RESULT 6
CQ896291
LOCUS       CQ896291                5832 bp    DNA     linear   PAT 05-NOV-2004
DEFINITION  Sequence 115 from Patent WO2004076614.
ACCESSION   CQ896291
VERSION     CQ896291.1  GI:55468140
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
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AUTHORS   Hinzmann,B., Dahl,E., Rosenthal,A., Specht,T., Schmitt,A.,
          Beckmann,G., Bruemmendorf,T., Kinnemann,H., Roepcke,S., Hermann,K.,
          Xinzhong,L., Pilarsky,C. and Staub,E.
TITLE     Human nucleic acid sequences obtained from prostatic carcinomas
JOURNAL   Patent: WO 2004076614-A 115 10-SEP-2004;
          Hinzmann, Bernd (DE); Dahl, Edgar (DE); Rosenthal, Andre (DE);
          Specht, Thomas (DE); Schmitt, Armin (DE)
FEATURES             Location/Qualifiers
     source          1. .5832
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              0            Length:          5832
Score:                  6779.00      Matches:         1323
Percent Similarity:     99.9%        Conservative:    1
Best Local Similarity:  99.8%        Mismatches:      1
Query Match:            99.9%        Indels:          0
DB:                     6            Gaps:            0

US-09-976-858-42 (1-1325) x CQ896291 (1-5832)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||
Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
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Db        476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
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Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db        596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Db        716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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Db        836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTGGGAAGTTGTTCTCATCA 895

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Db        896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Db        956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Db       1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Db       1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Db       1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Db       1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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Db       1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
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Db       1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
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Db       1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
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Db       1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
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Db       1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
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Db       1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Db       1676 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1735

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
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Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
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Db   1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy    621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Db   1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy    641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
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Qy    661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
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Qy    681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
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Db   2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy    701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Db   2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy    721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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Db   2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy    741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
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Db   2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy    761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
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Qy    781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Qy    801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Qy    841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Qy    861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
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Qy    881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
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Qy    901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Qy    921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
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Db   2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy    941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy    961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
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Db   2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy    981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
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Db   3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy   1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
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Db   3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy   1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
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Db   3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy   1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
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Qy   1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
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Qy   1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Qy   1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
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Db   3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy   1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
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Db   3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535

Qy   1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Qy   1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
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Db   3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy   1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
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Db   3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy   1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
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Qy   1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
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Qy   1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
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Db   3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy   1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
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Qy   1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
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Db   3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy   1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
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Db   4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy   1321 PheGluThrAlaLeu 1325
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Db   4076 TTCGAGACAGCACTG 4090
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RESULT 7
CS038316
LOCUS       CS038316                5871 bp    DNA     linear   PAT 10-MAR-2005
DEFINITION  Sequence 42 from Patent WO2005017121.
ACCESSION   CS038316
VERSION     CS038316.1  GI:60734839
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Francis-Lang,H., Winter,C.G., Ventura,R.B., Bjerke,L.M.,
            Lickteig,K., Adamkewicz,J.I., Zhang,H. and Hai,B.
  TITLE     Mbcats as modifiers of the beta-catenin pathway and methods of use
  JOURNAL   Patent: WO 2005017121-A 42 24-FEB-2005;
            Exelixis, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..5871
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ORIGIN

Alignment Scores:
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Score:                  6779.00      Matches:        1323
Percent Similarity:     99.9%        Conservative:   1
Best Local Similarity:  99.8%        Mismatches:     1
Query Match:            99.9%        Indels:         0
DB:                     6            Gaps:           0

US-09-976-858-42 (1-1325) x CS038316 (1-5871)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
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Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
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Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
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Db        236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Db        296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
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Db        356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
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Db        416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
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Db        476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
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Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db        596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
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Db        656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Db        716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Db        776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Db       1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Db       1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Db       1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Db       1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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Db       1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
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Db       1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
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Db       1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
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Db       1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
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Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
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Db       1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
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Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
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Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
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Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
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Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
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Db       2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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Db       2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
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Db       2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
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Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Db       2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
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Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
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Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
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Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
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Db       2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
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Db       2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
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Db       3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
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Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
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Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
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Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
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Db       3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
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Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
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Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
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Db        4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

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RESULT 8
CQ488793
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DEFINITION Sequence 20660 from Patent WO0160860.
ACCESSION   CQ488793
VERSION   CQ488793.1 GI:41454412
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schlegel,R., Endege,W.O. and Monahan,J.E.
  TITLE   Genes differentially expressed in human prostate cancer and their use
  JOURNAL   Patent: WO 0160860-A 20660 23-AUG-2001;
            Millennium Predictive Medicine, Inc. (US)
FEATURES   Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	4515
Score:	6770.00	Matches:	1324
Percent Similarity:	99.8%	Conservative:	0
Best Local Similarity:	99.8%	Mismatches:	1
Query Match:	99.7%	Indels:	1
DB:	6	Gaps:	0

US-09-976-858-42 (1-1325) x CQ488793 (1-4515)

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Qy           1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
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Db          99 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 158

Qy          21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         159 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 218

Qy          41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         219 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 278

Qy          61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Db         279 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 338

Qy          81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         339 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 398

Qy         101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         399 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 458

Qy         121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         459 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 518
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Qy         141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         519 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 578

Qy         161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db         579 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 638

Qy         181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
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Db         639 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 698

Qy         201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Db         699 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 758

Qy         221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         759 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 818

Qy         241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         819 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 878

Qy         261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Db         879 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 938

Qy         281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Db         939 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 998

Qy         301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Db         999 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1058

Qy         321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1059 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1118

Qy         341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Db        1119 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1178

Qy         361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1179 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1238

Qy         381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Db        1239 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1298

Qy         401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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Db        1299 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1358

Qy         421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1359 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1418

Qy         441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1419 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1478

Qy         461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1479 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1538

Qy         481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1539 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1598
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Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
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Db       1599 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1658

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1659 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1718

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1719 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1778

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Db       1779 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1838

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1839 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1898

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
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Db       1899 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1958

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Db       1959 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2018

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
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Db       2019 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2078

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
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Db       2079 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2138

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
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Db       2139 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2198

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Db       2199 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2258

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2259 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2318

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
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Db       2319 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2378

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2379 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2438

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Db       2439 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2498

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Db       2499 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2558

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Db       2559 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2618

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Db       2619 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2678

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
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Db       2679 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2738

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
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Db       2739 TATTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2798

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Db       2799 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2858

Qy        921 GluArgCysGlnGluLeuPheAspAlaHis-GlnAspLeuHisSerGluAlaTrpPheLe 940
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Db       2859 GAGAGGTGTCAGGAACTGTTTGATGCACACGCAGGATTTACATTCAGAGGCTTGGTTCTT 2918

Qy        940 uPheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVa 960
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Db       2919 GTTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGT 2978

Qy        960 lIleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGl 980
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Db       2979 CATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGG 3038

Qy        980 yLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSe 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3039 TTTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAG 3098

Qy       1000 rAlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGl 1020
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Db       3099 TGCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGA 3158

Qy       1020 uLysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVa 1040
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Db       3159 AAAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGT 3218

Qy       1040 lIleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHi 1060
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Db       3219 GATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCA 3278

Qy       1060 sLeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGl 1080
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Db       3279 TCTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGG 3338

Qy       1080 yLysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIl 1100
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Db       3339 AAAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGAT 3398

Qy       1100 eAspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIl 1120
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Qy       1120 eProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGl 1140
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Qy       1140 uHisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGl 1160
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Db       3519 GCACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGCACAACTTAAAGAAACCATTGA 3578

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Db       3579 AGATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGG 3638

Qy       1180 yGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIl 1200
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Db       3639 ACAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTAT 3698

Qy       1200 eAspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleAr 1220
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Db       3699 TGATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCG 3758

Qy       1220 gGluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAs 1240
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Db        3759 GGAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGA 3818

Qy        1240 pSerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVa 1260
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Db        3819 CAGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGT 3878

Qy        1260 lLeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGl 1280
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Db        3879 TTTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGA 3938

Qy        1280 uAlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIl 1300
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Db        3939 AGCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATAT 3998

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Db        3999 TGGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTAT 4058

Qy        1320 ePheGluThrAlaLeu 1325
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Db        4059 TTTCGAGACAGCACTG 4074

RESULT 9
CQ490536
LOCUS       CQ490536                4515 bp    DNA     linear   PAT 30-JAN-2004
DEFINITION  Sequence 22403 from Patent WO0160860.
ACCESSION   CQ490536
VERSION     CQ490536.1  GI:41456155
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schlegel,R., Endege,W.O. and Monahan,J.E.
  TITLE     Genes differentially expressed in human prostate cancer and their
            use
  JOURNAL   Patent: WO 0160860-A 22403 23-AUG-2001;
            Millennium Predictive Medicine, Inc. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
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Score:                  6770.00        Matches:         1324
Percent Similarity:     99.8%          Conservative:    0
Best Local Similarity:  99.8%          Mismatches:      1
Query Match:            99.7%          Indels:          1
DB:                     6              Gaps:            0

US-09-976-858-42 (1-1325) x CQ490536 (1-4515)

Qy           1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          99 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 158

Qy          21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
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Db         159 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 218

Qy          41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         219 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 278

Qy          61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Db         279 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 338

Qy          81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         339 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 398

Qy         101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
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Db         399 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 458

Qy         121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
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Db         459 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 518

Qy         141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db         579 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 638

Qy         181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
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Qy         201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Qy         221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Db         759 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 818

Qy         241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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Qy         261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Qy         281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Qy         301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Db         999 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1058

Qy         321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Db        1059 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1118

Qy         341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Db        1119 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1178

Qy         361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Qy         381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Qy         401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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Db        1299 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1358

Qy         421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
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Db        1359 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1418

Qy         441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
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Db       1419 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1478

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
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Db       1479 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1538

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
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Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
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Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Db       1659 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1718

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
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Db       1719 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1778

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Db       1779 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1838

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
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Db       2079 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2138

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
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Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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Db       2259 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2318

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
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Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
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Db       2379 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2438

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Qy        980 yLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSe 1000
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Qy       1000 rAlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGl 1020
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Qy       1020 uLysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVa 1040
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Db       3219 GATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCA 3278

Qy       1060 sLeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGl 1080
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Db       3279 TCTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGG 3338

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Qy       1100 eAspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIl 1120
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RESULT 10
CQ492310
LOCUS       CQ492310                4515 bp    DNA     linear   PAT 30-JAN-2004
DEFINITION  Sequence 24177 from Patent WO0160860.
ACCESSION   CQ492310
VERSION     CQ492310.1  GI:41457929
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schlegel,R., Endege,W.O. and Monahan,J.E.
  TITLE     Genes differentially expressed in human prostate cancer and their
            use
  JOURNAL   Patent: WO 0160860-A 24177 23-AUG-2001;
            Millennium Predictive Medicine, Inc. (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
Pred. No.:              0              Length:          4515
Score:                  6770.00        Matches:         1324
Percent Similarity:     99.8%          Conservative:    0
Best Local Similarity:  99.8%          Mismatches:      1
Query Match:            99.7%          Indels:          1
DB:                     6              Gaps:            0

US-09-976-858-42 (1-1325) x CQ492310 (1-4515)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
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Db         99 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 158

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Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
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Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
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Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Db        759 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 818

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 878

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 938

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Db        939 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 998

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Db        999 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1058

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1118

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1119 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1178

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Db       1179 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1238

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Db      1239 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1298

Qy       401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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Db      1299 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1358

Qy       421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
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Db      1359 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1418

Qy       441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
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Db      1419 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1478

Qy       461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
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Db      1479 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1538

Qy       481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
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Db      1539 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1598

Qy       501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
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Db      1599 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1658

Qy       521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Db      1659 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1718

Qy       541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
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Db      1719 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1778

Qy       561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Db      1779 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1838

Qy       581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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Db      1839 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1898

Qy       601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
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Db      1899 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1958

Qy       621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Db      1959 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2018

Qy       641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
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Db      2019 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2078

Qy       661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
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Db      2079 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2138

Qy       681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
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Db      2139 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2198

Qy       701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Db      2199 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2258

Qy       721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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Db      2259 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2318

Qy       741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
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Db      2319 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2378

Qy       761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2379 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2438

Qy       781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Db      2439 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2498

Qy       801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Db      2499 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2558

Qy       821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Db      2559 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2618

Qy       841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Db      2619 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2678

Qy       861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
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Db      2679 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2738

Qy       881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
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Db      2739 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2798

Qy       901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Db      2799 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2858

Qy       921 GluArgCysGlnGluLeuPheAspAlaHis-GlnAspLeuHisSerGluAlaTrpPheLe 940
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Db      2859 GAGAGGTGTCAGGAACTGTTTGATGCACACGCAGGATTTACATTCAGAGGCTTGGTTCTT 2918

Qy       940 uPheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVa 960
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Db      2919 GTTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGT 2978

Qy       960 lIleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGl 980
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Db      2979 CATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGG 3038

Qy       980 yLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSe 1000
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Db      3039 TTTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAG 3098

Qy      1000 rAlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGl 1020
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Db      3099 TGCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGA 3158

Qy      1020 uLysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVa 1040
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Db      3159 AAAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGT 3218

Qy      1040 lIleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHi 1060
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Db      3219 GATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCA 3278

Qy      1060 sLeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGl 1080
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Qy      1080 yLysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIl 1100
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Qy      1100 eAspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIl 1120
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Qy       1120 eProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGl 1140
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Db       3459 ACCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGA 3518

Qy       1140 uHisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGl 1160
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Db       3519 GCACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGCACAACTTAAAGAAACCATTGA 3578

Qy       1160 uAspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGl 1180
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Db       3579 AGATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGG 3638

Qy       1180 yGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIl 1200
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Db       3639 ACAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTAT 3698

Qy       1200 eAspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleAr 1220
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Qy       1220 gGluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAs 1240
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Qy       1240 pSerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVa 1260
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Db       3879 TTTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGA 3938

Qy       1280 uAlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIl 1300
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Db       3939 AGCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATAT 3998

Qy       1300 eGlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIl 1320
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Db       3999 TGGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTAT 4058

Qy       1320 ePheGluThrAlaLeu 1325
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Db       4059 TTTCGAGACAGCACTG 4074
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RESULT 11
CQ492702
LOCUS       CQ492702                4515 bp    DNA     linear   PAT 30-JAN-2004
DEFINITION  Sequence 24569 from Patent WO0160860.
ACCESSION   CQ492702
VERSION     CQ492702.1  GI:41458321
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schlegel,R., Endege,W.O. and Monahan,J.E.
  TITLE     Genes differentially expressed in human prostate cancer and their
            use
  JOURNAL   Patent: WO 0160860-A 24569 23-AUG-2001;
            Millennium Predictive Medicine, Inc. (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              0             Length:         4515
Score:                  6770.00       Matches:        1324
Percent Similarity:     99.8%         Conservative:   0
Best Local Similarity:  99.8%         Mismatches:     1
Query Match:            99.7%         Indels:         1
DB:                     6             Gaps:           0

US-09-976-858-42 (1-1325) x CQ492702 (1-4515)
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Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 158

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
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Db        159 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 218

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
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Db        219 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 278

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Db        279 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 338

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
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Db        339 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 398

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
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Db        399 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 458

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
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Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
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Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db        579 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 638

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
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Db        639 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 698

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Db        699 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 758

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Db        759 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 818

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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Db        819 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 878

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Db        879 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 938

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Db        939 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 998

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Db        999 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1058

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Db       1059 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1118
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Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Db       1119 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1178

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Db       1179 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1238

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Db       1239 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1298

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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Db       1299 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1358

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
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Db       1359 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1418

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
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Db       1419 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1478

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
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Db       1479 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1538

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
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Db       1539 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1598

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
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Db       1599 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1658

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Db       1659 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1718

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
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Db       1719 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1778

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Db       1779 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1838

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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Db       1839 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1898

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
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Db       1899 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1958

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Db       1959 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2018

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
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Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
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Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Db       2259 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2318

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
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Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
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Db       2379 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2438

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Db       2439 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2498

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Db       2619 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2678

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Db       2739 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2798

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Qy        960 lIleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGl 980
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Qy        980 yLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSe 1000
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Db       3039 TTTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAG 3098

Qy       1000 rAlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGl 1020
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Qy       1020 uLysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVa 1040
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Qy       1040 lIleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHi 1060
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Db       3219 GATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCA 3278

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Qy        1080 yLysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIl 1100
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Qy        1100 eAspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIl 1120
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Qy        1120 eProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGl 1140
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Qy        1140 uHisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGl 1160
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Qy        1160 uAspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGl 1180
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Db        3579 AGATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGG 3638

Qy        1180 yGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIl 1200
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Db        3639 ACAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTAT 3698

Qy        1200 eAspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleAr 1220
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Qy        1220 gGluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAs 1240
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Qy        1240 pSerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVa 1260
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Db        3879 TTTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGA 3938

Qy        1280 uAlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIl 1300
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Db        3939 AGCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATAT 3998

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Db        3999 TGGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTAT 4058

Qy        1320 ePheGluThrAlaLeu 1325
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RESULT 12
CQ494633
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DEFINITION  Sequence 26500 from Patent WO0160860.
ACCESSION   CQ494633
VERSION     CQ494633.1  GI:41460252
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schlegel,R., Endege,W.O. and Monahan,J.E.
  TITLE     Genes differentially expressed in human prostate cancer and their
            use
  JOURNAL   Patent: WO 0160860-A 26500 23-AUG-2001;
            Millennium Predictive Medicine, Inc. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              0              Length:         4515
Score:                  6770.00        Matches:        1324
Percent Similarity:     99.8%          Conservative:   0
Best Local Similarity:  99.8%          Mismatches:     1
Query Match:            99.7%          Indels:         1
DB:                     6              Gaps:           0

US-09-976-858-42 (1-1325) x CQ494633 (1-4515)

Qy           1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          99 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 158

Qy          21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
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Db         159 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 218

Qy          41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
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Db         219 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 278

Qy          61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Db         279 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 338

Qy          81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
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Qy         101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
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Db         399 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 458

Qy         121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
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Qy         141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
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Qy         161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Qy         181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
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Qy         201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Db         699 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 758

Qy         221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Qy         241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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Qy         261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Db         879 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 938
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Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Db       1059 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1118

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Db       1179 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1238

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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Db       1299 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1358

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
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Db       1359 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1418

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
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Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
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Db       1479 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1538

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
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Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
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Db       1599 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1658

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Db       1659 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1718

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
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Db       1719 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1778

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Db       1779 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1838

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
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Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Db       1959 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2018

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
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Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
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Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
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Db       2139 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2198

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
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Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
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Db       2379 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2438

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Db       2439 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2498

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
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Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Qy        980 yLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSe 1000
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Qy       1000 rAlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGl 1020
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Qy       1040 lIleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHi 1060
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Qy       1060 sLeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGl 1080
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Qy       1080 yLysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIl 1100
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Qy       1120 eProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGl 1140
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Qy       1160 uAspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGl 1180
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Db       3579 AGATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGG 3638

Qy       1180 yGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIl 1200
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Db       3639 ACAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTAT 3698

Qy       1200 eAspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleAr 1220
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Qy       1220 gGluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAs 1240
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Qy       1240 pSerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVa 1260
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Qy       1280 uAlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIl 1300
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Db       3939 AGCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATAT 3998

Qy       1300 eGlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIl 1320
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RESULT 13
CQ496370
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DEFINITION  Sequence 28237 from Patent WO0160860.
ACCESSION   CQ496370
VERSION     CQ496370.1  GI:41461989
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schlegel,R., Endege,W.O. and Monahan,J.E.
  TITLE     Genes differentially expressed in human prostate cancer and their
            use
  JOURNAL   Patent: WO 0160860-A 28237 23-AUG-2001;
            Millennium Predictive Medicine, Inc. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              0             Length:         4515
Score:                  6770.00       Matches:        1324
Percent Similarity:     99.8%         Conservative:   0
Best Local Similarity:  99.8%         Mismatches:     1
Query Match:            99.7%         Indels:         1
DB:                     6             Gaps:           0

US-09-976-858-42 (1-1325) x CQ496370 (1-4515)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
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Db         99 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 158

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
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Db        159 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 218

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
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Db        219 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 278

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Db        279 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 338

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
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Db        339 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 398

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
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Db        399 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 458

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Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db        579 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 638

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
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Db        639 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 698

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Db        699 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 758

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Qy          241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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Db          819 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 878

Qy          261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Qy          281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Qy          301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Db          999 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1058

Qy          321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Db         1059 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1118

Qy          341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Qy          361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Db         1179 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1238

Qy          381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Qy          401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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Db         1299 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1358

Qy          421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
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Db         1359 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1418

Qy          441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
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Qy          461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
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Qy          481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
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Db         1599 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1658

Qy          521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Qy          541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
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Qy          581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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Db         1839 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1898

Qy          601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
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Qy          621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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REFERENCE   1  (bases 1 to 5759)
  AUTHORS   Adachi,M., Sampath,J., Lan,L.B., Sun,D., Hargrove,P., Flatley,R.,
            Tatum,A., Edwards,M.Z., Wezeman,M., Matherly,L., Drake,R. and
            Schuetz,J.
  TITLE     Expression of MRP4 Confers Resistance to Ganciclovir and
            Compromises Bystander Cell Killing
  JOURNAL   J. Biol. Chem. 277 (41), 38998-39004 (2002)
   PUBMED   12105214
REFERENCE   2  (bases 1 to 5759)
  AUTHORS   Adachi,M., Sampath,J., Sun,D. and Schuetz,J.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-FEB-2002) Pharmaceutical Sciences, St. Jude
            Children's Research Hospital, 332 North Lauderdale St., Memphis, TN
            38105-2794, USA
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ORIGIN
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Db       1402 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1461

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
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Db       1462 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1521

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
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Db       1522 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1581

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Db       1582 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1641

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
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Db       1642 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1701

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Db       1702 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1761

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1762 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1821

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
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Db       1822 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1881

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Db       1882 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 1941

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
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Db       1942 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2001

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
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Db       2002 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2061
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Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
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Db       2062 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2121

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Db       2122 TATAAGAGTTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2181

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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Db       2182 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2241

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db       2242 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGGGAAGCTAGAT 2301

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
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Db       2302 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2361

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2362 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2421

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Db       2422 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2481

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Db       2482 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2541

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
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Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
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Db       2662 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGGATCTACAACTCGGAGTCCAGTG 2721

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
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Db       2842 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2901

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
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Db       2902 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 2961

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
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Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
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Db       3082 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3141

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
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Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
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Db       3202 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3261

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Db       3262 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3321

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
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Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
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Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
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Db       3502 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3561

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
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Db       3562 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3621

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
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Db       3622 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3681

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
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Db       3682 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3741

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
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Db       3742 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3801

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
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Db       3802 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3861

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
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Db       3862 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 3921

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
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Db       3922 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 3981

Qy       1321 PheGluThrAlaLeu 1325
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Db       3982 TTCGAGACAGCACTG 3996
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RESULT 15
AR278592
LOCUS       AR278592                6082 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 535 from patent US 6512094.
ACCESSION   AR278592
VERSION     AR278592.1  GI:29712838
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 6082)
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
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            Hepler,W.T. and Henderson,R.A.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: US 6512094-A 535 28-JAN-2003;
            Corixa Corporation; Seattle, WA
FEATURES             Location/Qualifiers
     source          1. .6082
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              0            Length:        6082
Score:                  6760.00      Matches:       1324
Percent Similarity:     99.9%        Conservative:  0
Best Local Similarity:  99.9%        Mismatches:    1
Query Match:            99.6%        Indels:        1
DB:                     6            Gaps:          0

US-09-976-858-42 (1-1325) x AR278592 (1-6082)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 245

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
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Db        246 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 305

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
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Db        306 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 365

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Db        366 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 425

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
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Db        426 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 485

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
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Db        486 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 545

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
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Db        546 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 605

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
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Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db        666 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 725

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
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Db        726 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 785

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Db        786 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 845

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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Db        906 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 965

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Db        966 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 1025

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Db       1026 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1085

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Db       1086 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1145

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Db       1266 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1325

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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Db       1386 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1445

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
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Db       1446 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1505

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
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Db       1506 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1565

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
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Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
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Db       1626 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1685

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
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Db       1686 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1745

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
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Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1926 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1985

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1986 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 2045

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
```

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2046 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2105

Qy         641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2106 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165

Qy         661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2166 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2225

Qy         681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2226 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2285

Qy         701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2286 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2345

Qy         721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2346 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2405

Qy         741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2406 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2465

Qy         761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2525

Qy         781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2526 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2585

Qy         801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2586 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2645

Qy         821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2646 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2705

Qy         841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2706 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2765

Qy         861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2766 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2825

Qy         881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2826 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2885

Qy         901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2886 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2945

Qy         921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2946 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 3005

Qy         941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3006 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 3065

Qy         961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3066 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3125

Qy         981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3126 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3185

Qy        1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3186 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3245

Qy        1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3246 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3305

Qy        1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3306 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3365

Qy        1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3366 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3425

Qy        1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3426 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3485

Qy        1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3486 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3545

Qy        1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3546 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3605

Qy        1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3606 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3665

Qy        1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3666 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3725

Qy        1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3726 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3785

Qy        1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
               ||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        3786 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAATC-CGG 3844

Qy        1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3845 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3904

Qy        1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3905 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3964

Qy        1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3965 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 4024

Qy        1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4025 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4084

Qy        1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4085 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4144

Qy        1321 PheGluThrAlaLeu 1325
               |||||||||||||||
Db        4145 TTCGAGACAGCACTG 4159
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Search completed: March 14, 2006, 13:44:34
Job time : 15594 secs

```
OM protein - nucleic search, using frame_plus_p2n model

Run on:         March 14, 2006, 07:38:05 ; Search time 1691 Seconds
                                           (without alignments)
                                           5222.187 Million cell updates/sec

Title:          US-09-976-858-42
Perfect score:  6787
Sequence:       1 MLPVYQEVKPNPLQDANLCS..........MVTNTSNGQPSTLTIFETAL 1325

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters:      9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US09976858/runat_13032006_170057_11733/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US09976858_@CGN_1_1_727_@runat_13032006_170057_11733 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      N_Geneseq_21:*
                1:  geneseqn1980s:*
                2:  geneseqn1990s:*
                3:  geneseqn2000s:*
                4:  geneseqn2001as:*
                5:  geneseqn2001bs:*
                6:  geneseqn2002as:*
                7:  geneseqn2002bs:*
                8:  geneseqn2003as:*
                9:  geneseqn2003bs:*
                10:  geneseqn2003cs:*
                11:  geneseqn2003ds:*
                12:  geneseqn2004as:*
                13:  geneseqn2004bs:*
                14:  geneseqn2005s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6787	100.0	3978	6	ABK92135	Abk92135 Prostate
2	6787	100.0	3978	11	ADN39251	Adn39251 Cancer/an
3	6785	99.9	5271	12	ADH10611	Adh10611 Human can
4	6785	99.9	5284	12	ADH10612	Adh10612 Human can
5	6785	99.9	5833	12	ADH10624	Adh10624 Human can
6	6785	99.9	5862	12	ADH10626	Adh10626 Human can
7	6781	99.9	4078	14	ADW14765	Adw14765 Tumor-ass
8	6779	99.9	4231	2	AAZ30078	Aaz30078 cDNA enco
9	6779	99.9	4231	5	AAH81778	Aah81778 Human dif
10	6779	99.9	4231	8	ABV75072	Abv75072 Human Dev
11	6779	99.9	4231	11	ADN39253	Adn39253 Cancer/an
12	6779	99.9	4231	14	ACL38944	Acl38944 ABCC4 cod
13	6779	99.9	4231	14	AEA00097	Aea00097 Human TAT
14	6779	99.9	4231	14	AEA00617	Aea00617 Human TAT
15	6779	99.9	5832	13	ADR66822	Adr66822 Human pro
16	6779	99.9	5832	13	ADR65919	Adr65919 Human pro
17	6779	99.9	5870	10	ADB75177	Adb75177 Prostate
18	6779	99.9	5871	14	ADX98506	Adx98506 Human ATP
19	6779	99.9	5871	14	ADZ49388	Adz49388 Insulin s
20	6770	99.7	4515	5	ABV24188	Abv24188 Human pro
21	6770	99.7	4515	5	ABV26511	Abv26511 Human pro
22	6770	99.7	4515	5	ABV20669	Abv20669 Human pro
23	6770	99.7	4515	5	ABV22410	Abv22410 Human pro
24	6770	99.7	4515	5	ABV24580	Abv24580 Human pro
25	6770	99.7	4515	5	ABV28224	Abv28224 Human pro
26	6760	99.6	6082	4	AAH93828	Aah93828 Human pro
27	6760	99.6	6082	4	AAS63921	Aas63921 Human pro
28	6760	99.6	6082	4	AAH85142	Aah85142 Human pro
29	6760	99.6	6082	5	ACA59729	Aca59729 Prostate
30	6760	99.6	6082	6	ABL95292	Abl95292 Human P51
31	6760	99.6	6082	8	ACC95456	Acc95456 Prostate
32	6760	99.6	6082	10	ADB13985	Adb13985 Human pro
33	6760	99.6	6082	10	ADG26401	Adg26401 Human pro
34	6647	97.9	3913	12	ADQ59423	Adq59423 Human can
35	6600.5	97.3	6140	4	AAH93829	Aah93829 Human pro
36	6600.5	97.3	6140	4	AAS63922	Aas63922 Human pro
37	6600.5	97.3	6140	4	AAH85143	Aah85143 Human pro
38	6600.5	97.3	6140	5	ACA59730	Aca59730 Prostate
39	6600.5	97.3	6140	6	ABL95293	Abl95293 Human P51
40	6600.5	97.3	6140	8	ACC95457	Acc95457 Prostate
41	6600.5	97.3	6140	10	ADB13986	Adb13986 Human pro
42	6600.5	97.3	6140	10	ADG26402	Adg26402 Human pro
43	6357	93.7	4395	8	ACC95747	Acc95747 Prostate
44	6357	93.7	4395	10	ADB14457	Adb14457 Expressio
45	6357	93.7	4395	10	ADG26980	Adg26980 Human pro

ALIGNMENTS

```
RESULT 1
ABK92135
ID   ABK92135 standard; DNA; 3978 BP.
XX
AC   ABK92135;
XX
DT   15-AUG-2002  (first entry)
XX
DE   Prostate cancer-associated DNA sequence #21.
XX
KW   Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW   gene therapy; gene; ds.
XX
OS   Mammalia.
XX
PN   WO200230268-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US032045.
XX
PR   13-OCT-2000; 2000US-00687576.
PR   08-DEC-2000; 2000US-00733288.
PR   08-DEC-2000; 2000US-00733742.
PR   24-JAN-2001; 2001US-0263957P.
PR   16-MAR-2001; 2001US-0276791P.
PR   16-MAR-2001; 2001US-0276888P.
PR   06-APR-2001; 2001US-0281922P.
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PR   24-APR-2001; 2001US-0286214P.
PR   30-APR-2001; 2001US-00847046.
PR   04-MAY-2001; 2001US-0288589P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Gish KC,  Mack DH,  Wilson KE,  Afar D,  Hevezi P;
XX
DR   WPI; 2002-471335/50.
DR   P-PSDB; ABG61820.
XX
PT   Detecting a prostate cancer-associated transcript in a cell in a patient,
PT   useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT   by determining if prostate cancer-associated genes are expressed in a
PT   prostate tissue.
XX
PS   Claim 22; Page 316; 436pp; English.
XX
CC   The present invention relates to methods of detecting a prostate cancer-
CC   associated transcript in a cell from a patient. The method comprises
CC   contacting a biological sample from the patient with prostate cancer-
CC   associated polynucleotides (designated PC genes) that selectively
CC   hybridise to a sequence that is at least 80% identical to them. The
CC   prostate cancer-associated polynucleotide sequences are differentially
CC   expressed in prostate tumour tissue or in prostate cancer and are derived
CC   from the tissues of various organisms such as humans or other mammals
CC   (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC   diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC   associated genes are useful for diagnosing or treating prostate cancer,
CC   as well as for identifying modulators of prostate cancer or agents that
CC   inhibit prostate cancer. The nucleic acid sequences are particularly
CC   useful in gene therapy, as a vaccine or in antisense applications.
CC   ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC   sequences
XX
SQ   Sequence 3978 BP; 1113 A; 817 C; 956 G; 1092 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0              Length:         3978
Score:                  6787.00        Matches:        1325
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     6              Gaps:           0

US-09-976-858-42 (1-1325) x ABK92135 (1-3978)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 60

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 120

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 180

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 240

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 300

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 360

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 420

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 480

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 540

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 600

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 660

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 720

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 780

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 840

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 900

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 960

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1020

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1080

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1140

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1200

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1260

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1320

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1380

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1440

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500
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Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1560

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1620

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1680

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1800

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1860

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 1920

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 1980

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2040

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2100

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2160

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2220

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2280

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2340

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2400

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2460

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2520

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2580

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2640

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2700

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2760

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2820

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2880

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 2940

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3000

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3060

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3120

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3180

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3240

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3300

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3360

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3420

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Db       3421 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3480

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3540

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3600

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3660

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3661 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3720

Qy        1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3721 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3780

Qy        1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3781 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3840

Qy        1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3841 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 3900

Qy        1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3901 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 3960

Qy        1321 PheGluThrAlaLeu 1325
               |||||||||||||||
Db        3961 TTCGAGACAGCACTG 3975

RESULT 2
ADN39251
ID   ADN39251 standard; cDNA; 3978 BP.
XX
AC   ADN39251;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:569.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003042661-A2.
XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036810.
XX
PR   13-NOV-2001; 2001US-0350666P.
PR   21-NOV-2001; 2001US-0332464P.
PR   29-NOV-2001; 2001US-0334393P.
PR   03-DEC-2001; 2001US-0335394P.
PR   14-DEC-2001; 2001US-0340376P.
PR   08-JAN-2002; 2002US-0347211P.
PR   10-JAN-2002; 2002US-0347349P.
PR   08-FEB-2002; 2002US-0355250P.
PR   13-FEB-2002; 2002US-0356714P.
PR   20-FEB-2002; 2002US-0359077P.
PR   29-MAR-2002; 2002US-0368809P.
PR   04-APR-2002; 2002US-0370110P.
PR   12-APR-2002; 2002US-0372246P.
PR   05-JUN-2002; 2002US-0386614P.
PR   16-JUL-2002; 2002US-0396839P.
PR   22-JUL-2002; 2002US-0397775P.
PR   22-JUL-2002; 2002US-0397845P.
PR   09-SEP-2002; 2002US-0409450P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D,  Aziz N,  Ginsburg WM,  Gish KC,  Glynne R,  Hevezi PA;
PI   Mack DH,  Murray R,  Watson SR,  Wilson KE,  Zlotnik A;
XX
DR   WPI; 2003-468649/44.
DR   P-PSDB; ADN39252.
XX
PT   Determining the presence or absence of a pathological cell in a patient,
PT   useful for diagnosing, prognosing or treating cancer, comprises detecting
PT   a nucleic acid in a biological sample.
XX
PS   Claim 8; SEQ ID NO 569; 1385pp; English.
XX
CC   The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC   whose expression is upregulated or downregulated in specific cancers or
CC   other diseases such as angiogenic or fibrotic disorders, and to methods
CC   of determining the presence or absence of a pathological cell in a
CC   patient by detecting a nucleic acid at least 80% identical to those of
CC   the invention or by detecting a polypeptide of the invention. The
CC   invention also relates to expression vectors and host cells comprising a
CC   nucleic acid of the invention; antibodies which specifically bind a
CC   polypeptide of the invention; use of such antibodies for drug targeting;
CC   and methods of screening for modulators of activity or expression of the
CC   polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC   antibodies and methods are useful for diagnosing, prognosing and treating
CC   cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC   atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC   neovascularistaion syndromes, scarring and uterine fibroids. They may
CC   also be useful in wound healing and in contraception. The present
CC   sequence represents a nucleic acid sequence of the invention.
XX
SQ   Sequence 3978 BP; 1113 A; 817 C; 956 G; 1092 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                0              Length:        3978
Score:                    6787.00        Matches:       1325
Percent Similarity:       100.0%         Conservative:  0
Best Local Similarity:    100.0%         Mismatches:    0
Query Match:              100.0%         Indels:        0
DB:                       11             Gaps:          0

US-09-976-858-42 (1-1325) x ADN39251 (1-3978)

Qy           1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 60

Qy          21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 120

Qy          41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 180

Qy          61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 240

Qy          81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 300

Qy         101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 360

Qy         121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 420

Qy         141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 480

Qy         161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        481 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 540

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 600

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 660

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 720

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 780

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 840

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 900

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 960

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1020

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1080

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1140

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1200

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1260

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1320

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1380

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1440

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1560

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1620

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1680

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1800

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1860

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 1920

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 1980

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2040

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2100

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2160

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2220

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2280

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2340

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2400

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2460

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2520

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2580

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2640

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2700
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Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 TTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2760

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2820

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2880

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 2940

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3000

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3060

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3120

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3180

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3240

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3300

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3360

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3420

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3480

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3540

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3600

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3660

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3720

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3780

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3840

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 3900

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 3960

Qy       1321 PheGluThrAlaLeu 1325
              |||||||||||||||
Db       3961 TTCGAGACAGCACTG 3975
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RESULT 3
ADH10611

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ID   ADH10611 standard; DNA; 5271 BP.
XX
AC   ADH10611;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human cancer-related polynucleotide, SEQ ID 1.
XX
KW   Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003104404-A2.
XX
PD   18-DEC-2003.
XX
PF   05-JUN-2003; 2003WO-US017772.
XX
PR   06-JUN-2002; 2002US-0386651P.
XX
PA   (AVAL-) AVALON PHARM INC.
XX
PI   Ebner R;
XX
DR   WPI; 2004-062332/06.
XX
PT   Identifying agents that modulate the activity of cancer-related gene,
PT   useful for treating or diagnosing prostate cancer comprising contacting a
PT   compound with a cell containing a gene under conditions promoting
PT   expression of the gene.
XX
PS   Claim 1; SEQ ID NO 1; 79pp; English.
XX
CC   The invention relates to identifying an agent that modulates the activity
CC   of a cancer-related gene. The method involves contacting a compound with
CC   a cell containing a gene that corresponds to a polynucleotide having a
CC   sequence selected from (SEQ ID NO. 1-18) under conditions promoting the
CC   expression of the gene. The method is useful for identifying an agent
CC   that modulates the activity of a cancer-related gene. The polypeptides
CC   and antibodies of the invention are useful for treating and diagnosing
CC   cancer, preferably prostate cancer. It is also useful for screening
CC   assays for agents that are effective in reducing the activity of cancer-
CC   related genes. The present sequence represents a specific example of a
CC   cancer-related polynucleotide sequence.
XX
SQ   Sequence 5271 BP; 1480 A; 1087 C; 1212 G; 1492 T; 0 U; 0 Other;
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Alignment Scores:

Pred. No.:	0	Length:	5271
Score:	6785.00	Matches:	1324
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	99.9%	Mismatches:	0
Query Match:	99.9%	Indels:	0
DB:	12	Gaps:	0

US-09-976-858-42 (1-1325) x ADH10611 (1-5271)

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Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1676 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1735

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1736 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1795

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1856 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2096 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2155

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy         741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy         761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455

Qy         781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2515

Qy         801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2516 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575

Qy         821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy         841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695

Qy         861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2696 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2755

Qy         881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815

Qy         901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2816 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875

Qy         921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy         941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy         961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy         981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy        1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy        1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy        1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy        1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355

Qy        1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy        1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy        1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3535

Qy        1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595

Qy        1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy        1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy        1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy        1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy        1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy        1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy        1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy        1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy        1321 PheGluThrAlaLeu 1325
               |||||||||||||||
Db        4076 TTCGAGACAGCACTG 4090
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RESULT 4
ADH10612
ID   ADH10612 standard; DNA; 5284 BP.
XX
AC   ADH10612;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human cancer-related polynucleotide, SEQ ID 2.
XX
KW   Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003104404-A2.
XX
PD   18-DEC-2003.
XX
PF   05-JUN-2003; 2003WO-US017772.
XX
PR   06-JUN-2002; 2002US-0386651P.
XX
PA   (AVAL-) AVALON PHARM INC.
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XX
PI   Ebner R;
XX
DR   WPI; 2004-062332/06.
XX
PT   Identifying agents that modulate the activity of cancer-related gene,
PT   useful for treating or diagnosing prostate cancer comprising contacting a
PT   compound with a cell containing a gene under conditions promoting
PT   expression of the gene.
XX
PS   Claim 1; SEQ ID NO 2; 79pp; English.
XX
CC   The invention relates to identifying an agent that modulates the activity
CC   of a cancer-related gene. The method involves contacting a compound with
CC   a cell containing a gene that corresponds to a polynucleotide having a
CC   sequence selected from (SEQ ID NO. 1-18) under conditions promoting the
CC   expression of the gene. The method is useful for identifying an agent
CC   that modulates the activity of a cancer-related gene. The polypeptides
CC   and antibodies of the invention are useful for treating and diagnosing
CC   cancer, preferably prostate cancer. It is also useful for screening
CC   assays for agents that are effective in reducing the activity of cancer-
CC   related genes. The present sequence represents a specific example of a
CC   cancer-related polynucleotide sequence.
XX
SQ   Sequence 5284 BP; 1480 A; 1138 C; 1210 G; 1456 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:               0             Length:         5284
Score:                   6785.00       Matches:        1324
Percent Similarity:      100.0%        Conservative:   1
Best Local Similarity:   99.9%         Mismatches:     0
Query Match:             99.9%         Indels:         0
DB:                      12            Gaps:           0

US-09-976-858-42 (1-1325) x ADH10612 (1-5284)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1676 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1735

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1736 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1795

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1856 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2096 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2155

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2515

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2516 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2696 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2755

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2816 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3535

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955
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Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy       1321 PheGluThrAlaLeu 1325
              |||||||||||||||
Db       4076 TTCGAGACAGCACTG 4090

RESULT 5
ADH10624
ID   ADH10624 standard; DNA; 5833 BP.
XX
AC   ADH10624;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human cancer-related polynucleotide, SEQ ID 14.
XX
KW   Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003104404-A2.
XX
PD   18-DEC-2003.
XX
PF   05-JUN-2003; 2003WO-US017772.
XX
PR   06-JUN-2002; 2002US-0386651P.
XX
PA   (AVAL-) AVALON PHARM INC.
XX
PI   Ebner R;
XX
DR   WPI; 2004-062332/06.
XX
PT   Identifying agents that modulate the activity of cancer-related gene,
PT   useful for treating or diagnosing prostate cancer comprising contacting a
PT   compound with a cell containing a gene under conditions promoting
PT   expression of the gene.
XX
PS   Claim 1; SEQ ID NO 14; 79pp; English.
XX
CC   The invention relates to identifying an agent that modulates the activity
CC   of a cancer-related gene. The method involves contacting a compound with
CC   a cell containing a gene that corresponds to a polynucleotide having a
CC   sequence selected from (SEQ ID NO. 1-18) under conditions promoting the
CC   expression of the gene. The method is useful for identifying an agent
CC   that modulates the activity of a cancer-related gene. The polypeptides
CC   and antibodies of the invention are useful for treating and diagnosing
CC   cancer, preferably prostate cancer. It is also useful for screening
CC   assays for agents that are effective in reducing the activity of cancer-
CC   related genes. The present sequence represents a specific example of a
CC   cancer-related polynucleotide sequence.
XX
SQ   Sequence 5833 BP; 1660 A; 1175 C; 1306 G; 1692 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0            Length:         5833
Score:                  6785.00      Matches:        1324
Percent Similarity:     100.0%       Conservative:   1
Best Local Similarity:  99.9%        Mismatches:     0
Query Match:            99.9%        Indels:         0
DB:                     12           Gaps:           0

US-09-976-858-42 (1-1325) x ADH10624 (1-5833)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255
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Qy     381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy     401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy     421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy     441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy     461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy     481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615

Qy     501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy     521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1676 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1735

Qy     541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1736 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1795

Qy     561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855

Qy     581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1856 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915

Qy     601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy     621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy     641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095

Qy     661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2096 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2155

Qy     681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy     701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy     721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy     741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy     761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455

Qy     781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2515

Qy     801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2516 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575

Qy     821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy     841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695

Qy     861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2696 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2755

Qy     881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815

Qy     901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2816 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875

Qy     921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy     941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy     961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy     981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy    1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy    1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy    1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
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Db    3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy    1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355

Qy    1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy    1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy         1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3535

Qy         1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Db         3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595

Qy         1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy         1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy         1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy         1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy         1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy         1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy         1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy         1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy         1321 PheGluThrAlaLeu 1325
                |||||||||||||||
Db         4076 TTCGAGACAGCACTG 4090
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RESULT 6
ADH10626

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ID   ADH10626 standard; DNA; 5862 BP.
XX
AC   ADH10626;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human cancer-related polynucleotide, SEQ ID 16.
XX
KW   Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003104404-A2.
XX
PD   18-DEC-2003.
XX
PF   05-JUN-2003; 2003WO-US017772.
XX
PR   06-JUN-2002; 2002US-0386651P.
XX
PA   (AVAL-) AVALON PHARM INC.
XX
PI   Ebner R;
XX
DR   WPI; 2004-062332/06.
XX
PT   Identifying agents that modulate the activity of cancer-related gene,
PT   useful for treating or diagnosing prostate cancer comprising contacting a
PT   compound with a cell containing a gene under conditions promoting
PT   expression of the gene.
XX
PS   Claim 1; SEQ ID NO 16; 79pp; English.
XX
CC   The invention relates to identifying an agent that modulates the activity
CC   of a cancer-related gene. The method involves contacting a compound with
CC   a cell containing a gene that corresponds to a polynucleotide having a
CC   sequence selected from (SEQ ID NO. 1-18) under conditions promoting the
CC   expression of the gene. The method is useful for identifying an agent
CC   that modulates the activity of a cancer-related gene. The polypeptides
CC   and antibodies of the invention are useful for treating and diagnosing
CC   cancer, preferably prostate cancer. It is also useful for screening
CC   assays for agents that are effective in reducing the activity of cancer-
CC   related genes. The present sequence represents a specific example of a
CC   cancer-related polynucleotide sequence.
XX
SQ   Sequence 5862 BP; 1645 A; 1208 C; 1328 G; 1681 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:               0             Length:          5862
Score:                   6785.00       Matches:         1324
Percent Similarity:      100.0%        Conservative:    1
Best Local Similarity:   99.9%         Mismatches:      0
Query Match:             99.9%         Indels:          0
DB:                      12            Gaps:            0

US-09-976-858-42 (1-1325) x ADH10626 (1-5862)

Qy            1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
                |||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db          116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy           21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy           41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy           61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy           81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy          101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy          121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy          141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy          161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy          181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715
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Qy    201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy    221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy    241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy    261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy    281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy    301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy    321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy    341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy    361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy    381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy    401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy    421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy    441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy    461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy    481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615

Qy    501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy    521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1676 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1735

Qy    541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
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Db   1736 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1795

Qy    561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855

Qy    581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1856 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915

Qy    601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy    621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy    641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095

Qy    661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2096 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2155

Qy    681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy    701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Db   2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy    721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy    741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy    761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455

Qy    781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2515

Qy    801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Db   2516 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575

Qy    821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Db   2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy    841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Db   2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695

Qy    861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
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Db   2696 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2755

Qy    881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
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Db   2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815

Qy    901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Db   2816 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875

Qy    921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
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Db       2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
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Db       3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
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Db       3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
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Db       3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
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Db       3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
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Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Db       3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
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Db       3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
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Db       3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3535

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Db       3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
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Db       3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
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Db       3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
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Db       3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
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Db       3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
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Db       3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
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Db       3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
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Db       3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
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Db       4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy       1321 PheGluThrAlaLeu 1325
              |||||||||||||||
Db       4076 TTCGAGACAGCACTG 4090
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RESULT 7
ADW14765
ID   ADW14765 standard; cDNA; 4078 BP.
XX
AC   ADW14765;
XX
DT   07-APR-2005  (first entry)
XX
DE   Tumor-associated antigenic target TAT425 cDNA clone DNA340411.
XX
KW   Tumor-associated antigenic target; TAT425; cancer; neoplasm; cytostatic;
KW   renal tumor; uterus tumor; prostate tumor; pancreas tumor; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             8. .3985
FT                   /*tag=  a
FT                   /product= "TAT425"
FT                   /transl_except= (pos:2630. .2632,aa:Phe)
XX
PN   WO2005003154-A2.
XX
PD   13-JAN-2005.
XX
PF   02-JUL-2004; 2004WO-US021353.
XX
PR   02-JUL-2003; 2003US-0484959P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi A,  Cairns B,  Dowd P,  Frantz G,  French D,  Gonzalez L;
PI   Polakis P,  Smith V,  Wolf B,  Wu TD,  Zhang Z;
XX
DR   WPI; 2005-091764/10.
DR   P-PSDB; ADW14772.
XX
PT   New Tumor-associated Antigenic Target polypeptides useful for diagnosing,
PT   preventing or treating cell proliferative disorders such as cancer or
PT   tumor.
XX
PS   Claim 1; SEQ ID NO 3; 141pp; English.
XX
CC   The present sequence is that of cDNA clone DNA340411 encoding novel tumor
CC   -associated antigenic target polypeptide TAT425. TAT polypeptides have
CC   been identified ADW14770-ADW14776 whose expression is upregulated in
CC   particular tumor tissues. Tissue expression profiling using GeneExpress
CC   indicated that TAT425 is upregulated in kidney tumor and prostate tumor
CC   tissues as compared to the corresponding healthy tissues. Upregulation in
CC   prostate tumor tissue was confirmed by quantitative analysis of TAT mRNA
CC   expression, and results were confirmed by gene expression profiling in
CC   silico (GEPIS) analysis which also indicated upregulation in uterus tumor
CC   and pancreas tumor tissues. The TAT polypeptide may comprise the full-
CC   length polypeptide, or the extracellular domain, and may be fused to a
CC   heterologous polypeptide such as an epitope tag, or the Fc region of an
CC   immunoglobulin. TAT polypeptides of the invention, and their encoding
CC   nucleic acids, provide targets for the diagnosis and therapy of cancer.
XX
SQ   Sequence 4078 BP; 1141 A; 839 C; 979 G; 1119 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0            Length:        4078
Score:                  6781.00      Matches:       1324
Percent Similarity:     99.9%        Conservative:  0
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Best Local Similarity:  99.9%        Mismatches:   1
Query Match:            99.9%        Indels:       0
DB:                     14           Gaps:         0

US-09-976-858-42 (1-1325) x ADW14765 (1-4078)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 67

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 127

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 187

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Db        188 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 247

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
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Db        248 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 307

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 367

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
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Db        368 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 427

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 487

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db        488 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 547

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 607

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Db        608 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 667

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Db        668 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 727

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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Db        728 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 787

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Db        788 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 847

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Db        848 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 907

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Db        908 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 967

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1027

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Db       1028 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1087

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Db       1088 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1147

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Db       1148 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1207

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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Db       1208 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1267

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
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Db       1268 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1327

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1328 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1387

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
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Db       1388 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1447

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
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Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1567

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Db       1568 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1627

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1628 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1687

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1688 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1747

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1748 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1807

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
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Db       1808 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1867

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Db       1868 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 1927

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1928 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 1987

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1988 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2047

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
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Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Db       2108 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2167

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2168 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2227

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2228 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2287

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2288 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2347

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Db       2348 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2407

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Db       2408 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2467

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Db       2468 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2527

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Db       2528 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2587

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
              ||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||
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Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
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Db       2648 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2707

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
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Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
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Db       2828 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2887

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
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Db       2888 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 2947

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
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Db       2948 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3007

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
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Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
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Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
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Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
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Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
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Db       3308 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3367

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
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Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Db       3428 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3487

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
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Db       3488 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3547

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
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Db       3548 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3607

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
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Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
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Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
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Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
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Db       3788 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3847

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
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Db       3848 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 3907

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
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Db       3908 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 3967

Qy       1321 PheGluThrAlaLeu 1325
              |||||||||||||||
Db       3968 TTCGAGACAGCACTG 3982
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RESULT 8
AAZ30078
ID   AAZ30078 standard; cDNA; 4231 BP.
XX
AC   AAZ30078;
XX
DT   26-JAN-2000  (first entry)
XX
DE   cDNA encoding a human MPR-related ABC transporter designated MOAT-B.
XX
KW   Human; MPR-related ABC transporter; MOAT protein; MOAT-B;
KW   MOAT mediated transport; anticancer drug sensitivity;
KW   transporter mediated cellular efflux; anticancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             116..4093
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FT                   /product= "MOAT-B"
FT                   /transl_except= (pos: 1715. .1717, aa: Pro)
FT                   /transl_except= (pos: 3566. .3568, aa: Arg)
FT                   /note= "MPR-related ABC transporter"
XX
PN   WO9949735-A1.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006644.
XX
PR   27-MAR-1998;   98US-0079759P.
PR   03-AUG-1998;   98US-0095153P.
XX
PA   (FOXC-) FOX CHASE CANCER CENT.
XX
PI   Kruh G,  Lee K,  Belinsky M,  Bain L;
XX
DR   WPI; 1999-610812/52.
DR   P-PSDB; AAY43541.
XX
PT   New transporter gene useful for screening for anti-cancer drugs.
XX
PS   Claim 1; Page 130-131; 153pp; English.
XX
CC   The present sequence encodes a human MPR-related ABC transporter (MOAT)
CC   protein, designated MOAT-B. The protein comprises a multi-domain
CC   structure including a tandem repeat of nucleotide binding folds appended
CC   C-terminal to a hydrophobic domain, having Walker A and B ATP binding
CC   sites and several potential membrane spanning domains. The MOAT nucleic
CC   acids are useful for screening a test compound for inhibition of MOAT
CC   mediated transport, indicated by restoration of anticancer drug
CC   sensitivity, which in turn causes a reduction of transporter mediated
CC   cellular efflux of anticancer agents. MOAT DNA or RNA may be used as
CC   probes to detect the presence or expression of genes encoding MOAT
CC   proteins. Anti-MOAT antibodies are useful for detecting and quantitating
CC   MOAT proteins
XX
SQ   Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0             Length:        4231
Score:                  6779.00       Matches:       1323
Percent Similarity:     99.9%         Conservative:  1
Best Local Similarity:  99.8%         Mismatches:    1
Query Match:            99.9%         Indels:        0
DB:                     2             Gaps:          0

US-09-976-858-42 (1-1325) x AAZ30078 (1-4231)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Db        296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
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Db        536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db        596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Db        716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Db        776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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Db        836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Db        896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Db        956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Db       1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Db       1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Db       1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Db       1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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Db       1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
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Db       1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
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Db       1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
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Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
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Db       1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
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Db       1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
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Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Db       1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1856 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2096 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2155

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2515

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2516 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2696 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2755

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2816 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||. |||
Db       3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy        1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy        1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy        1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy        1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy        1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy        1321 PheGluThrAlaLeu 1325
                |||||||||||||||
Db        4076 TTCGAGACAGCACTG 4090
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RESULT 9
AAH81778
ID   AAH81778 standard; DNA; 4231 BP.
XX
AC   AAH81778;
XX
DT   21-SEP-2001  (first entry)
XX
DE   Human differential transcription-associated cDNA SEQ ID 287.
XX
KW   Differential transcription; human; rat; tumour cell; cytostatic;
KW   Ras modulator; Class II tumour suppressor gene; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157058-A2.
XX
PD   09-AUG-2001.
XX
PF   31-JAN-2001; 2001WO-EP001003.
XX
PR   31-JAN-2000; 2000DE-01004102.
XX
PA   (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI   Rosenthal A,  Hinzmann B,  Schaefer R,  Zuber J,  Tchernitsa O;
PI   Grips M,  Hellriegel M,  Schmitz A,  Sers C;
XX
DR   WPI; 2001-483415/52.
XX
PT   Nucleic acids differentially expressed between tumor and normal cells,
PT   useful for diagnosis or therapy of tumors and for screening active
PT   agents.
XX
PS   Disclosure; Page 442-443; 579pp; German.
XX
CC   This invention describes a nucleic acid (I) with differential expression
CC   between tumour and normal cells and which has cytostatic activity. (I)
CC   work as modulators of Ras activity by inducing expression of tumour
CC   suppressor genes. (I), and polypeptides encoded by them, are useful as
CC   targets for diagnosis or therapy and in screening to determine the
CC   effects of an active compound (potential pharmaceutical) on a cell line,
CC   particularly for diagnosis and treatment of tumors, especially by
CC   modulating expression of (I) (by gene therapy, antisense RNA or ribozyme
CC   methods) or by modulating the amount and/or location of (I)-encoded
CC   polypeptides (by administration of the polypeptide or its activator,
CC   antibody (optionally as a conjugate) or inhibitor). The method allows
CC   identification of many Class II tumour suppressor genes (i.e. genes that
CC   are not primary targets for tumour-initiating mutations). AAH81492-
CC   AAH82376 represent the human and rat derived nucleic acid fragments
CC   described in the method of the invention
XX
SQ   Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0           Length:         4231
Score:                  6779.00     Matches:        1323
Percent Similarity:     99.9%       Conservative:   1
Best Local Similarity:  99.8%       Mismatches:     1
Query Match:            99.9%       Indels:         0
DB:                     5           Gaps:           0

US-09-976-858-42 (1-1325) x AAH81778 (1-4231)

Qy           1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
               |||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db         116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy          21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy          41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy          61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy          81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy         101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy         121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy         141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy         161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy         181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy         201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy         221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy         241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy         261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955
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Qy       281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy       301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy       321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy       341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy       361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy       381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy       401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy       421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy       441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy       461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy       481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTGGGAAGAAATATGAA 1615

Qy       501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy       521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1676 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1735

Qy       541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1736 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1795

Qy       561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855

Qy       581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1856 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915

Qy       601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy       621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy       641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095

Qy       661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2096 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2155

Qy       681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy       701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy       721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy       741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy       761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455

Qy       781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2515

Qy       801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2516 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575

Qy       821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy       841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695

Qy       861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2696 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2755

Qy       881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815

Qy       901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2816 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875

Qy       921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy       941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy       961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy       981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy      1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy       1321 PheGluThrAlaLeu 1325
              |||||||||||||||
Db       4076 TTCGAGACAGCACTG 4090

RESULT 10
ABV75072
ID   ABV75072 standard; DNA; 4231 BP.
XX
AC   ABV75072;
XX
DT   19-FEB-2003  (first entry)
XX
DE   Human DevG4 homologue protein encoding DNA.
XX
KW   Protein disulfide isomerase; DevG20; ABC transporter; DevG4; DevG22;
KW   anorectic; immunomodulator; antidepressant; antidiabetic; hypotensive;
KW   antiarteriosclerotic; antilipemic; osteopathic; antiarthritic; gene;
KW   litholytic; hepatotropic; cytostatic; neuroprotective; gene therapy;
KW   transgenic; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             115..4092
FT                   /*tag=  a
FT                   /product= "DevG4 homologue protein"
XX
PN   WO200279238-A2.
XX
PD   10-OCT-2002.
XX
PF   28-MAR-2002; 2002WO-EP003540.
XX
PR   02-APR-2001; 2001EP-00108315.
PR   01-JUN-2001; 2001EP-00113419.
XX
PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
XX
PI   Eulenberg K,  Broenner G,  Ciossek T,  Haeder T,  Steuernagel A;
XX
DR   WPI; 2003-067420/06.
DR   P-PSDB; ABB82645.
XX
PT   New protein disulfide isomerase and ABC transporter nucleic acids or
PT   polypeptides, useful for diagnosing, treating or preventing obesity,
PT   hypertension, heart disease, hypercholesterolemia, osteoarthritis,
PT   gallstones or cancer.
XX
PS   Claim 2; Fig 9C; 99pp; English.
XX
CC   The invention relates to pharmaceutical composition comprising carriers,
CC   diluents and/or adjuvants, with any of: (a) a nucleic acid molecule of
CC   the protein disulfide isomerase (DevG20) or ABC transporter (DevG4 or
CC   DevG22) gene family; (b) a polypeptide encoded by (a); (c) a fragment or
CC   variant of (a) or (b); or (d) an antibody, an aptamer or another receptor
CC   recognizing (a) or (b). The composition is useful for manufacturing an
CC   agent for detecting and/or verifying, diagnosing, treating, alleviating
CC   or preventing a metabolic disorder, e.g. obesity, adipositas, eating/body
CC   weight disorders, cachexia (wasting), pancreatic dysfunction (diabetes
CC   mellitus), hypertension, arteriosclerosis, coronary artery disease (CAD),
CC   coronary heart disease, hypercholesterolemia, dyslipidemia,
CC   osteoarthritis, gallstones, cancer (cancer of the reproductive organs),
CC   sleep apnea, disorders related to ROS production and neurodegenerative
CC   diseases in cells, cell masses, organs and/or subjects. The inhibitors,
CC   modulators or agents identified above are useful for treating, preventing
CC   or alleviating the diseases mentioned. The nucleic acid molecule of
CC   DevG20, DevG4 and/or Dev is also useful for preparing a non-human animal
CC   which over- or underexpresses the DevG20, DevG4 and/or Dev gene product.
CC   The present sequence represents a DNA encoding a human DevG4 homologue
CC   protein, a ATP-binding cassette, sub family C (CFTR/MRP), member 4, also
CC   referred to as ABCC4 and MPR4 (Gen Bank Accn No. NM_005845)
XX
SQ   Sequence 4231 BP; 1170 A; 894 C; 1016 G; 1151 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0              Length:         4231
Score:                  6779.00        Matches:        1323
Percent Similarity:     99.9%          Conservative:   1
Best Local Similarity:  99.8%          Mismatches:     1
Query Match:            99.9%          Indels:         0
DB:                     8              Gaps:           0

US-09-976-858-42 (1-1325) x ABV75072 (1-4231)
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Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 ATGGCAGTTCTAATCATTCTGCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195
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Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1676 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1735

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1736 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1795

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1856 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2096 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2155

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy         741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy         761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455

Qy         781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2515

Qy         801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2516 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575

Qy         821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy         841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695

Qy         861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2696 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2755

Qy         881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815

Qy         901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2816 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875

Qy         921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy         941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy         961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy         981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy        1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy        1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy        1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy        1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355

Qy        1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy        1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy        1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535

Qy        1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Db        3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595

Qy        1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy        1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy        1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy        1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy        1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy        1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy        1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy        1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy        1321 PheGluThrAlaLeu 1325
               ||||||||||||||
Db        4076 TTCGAGACAGCACTG 4090
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RESULT 11
ADN39253
ID   ADN39253 standard; cDNA; 4231 BP.
XX
AC   ADN39253;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:571.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003042661-A2.
XX
PD   22-MAY-2003.
```

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XX
PF   13-NOV-2002; 2002WO-US036810.
XX
PR   13-NOV-2001; 2001US-0350666P.
PR   21-NOV-2001; 2001US-0332464P.
PR   29-NOV-2001; 2001US-0334393P.
PR   03-DEC-2001; 2001US-0335394P.
PR   14-DEC-2001; 2001US-0340376P.
PR   08-JAN-2002; 2002US-0347211P.
PR   10-JAN-2002; 2002US-0347349P.
PR   08-FEB-2002; 2002US-0355250P.
PR   13-FEB-2002; 2002US-0356714P.
PR   20-FEB-2002; 2002US-0359077P.
PR   29-MAR-2002; 2002US-0368809P.
PR   04-APR-2002; 2002US-0370110P.
PR   12-APR-2002; 2002US-0372246P.
PR   05-JUN-2002; 2002US-0386614P.
PR   16-JUL-2002; 2002US-0396839P.
PR   22-JUL-2002; 2002US-0397775P.
PR   22-JUL-2002; 2002US-0397845P.
PR   09-SEP-2002; 2002US-0409450P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D,  Aziz N,  Ginsburg WM,  Gish KC,  Glynne R,  Hevezi PA;
PI   Mack DH,  Murray R,  Watson SR,  Wilson KE,  Zlotnik A;
XX
DR   WPI; 2003-468649/44.
DR   P-PSDB; ADN39254.
XX
PT   Determining the presence or absence of a pathological cell in a patient,
PT   useful for diagnosing, prognosing or treating cancer, comprises detecting
PT   a nucleic acid in a biological sample.
XX
PS   Claim 8; SEQ ID NO 571; 1385pp; English.
XX
CC   The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC   whose expression is upregulated or downregulated in specific cancers or
CC   other diseases such as angiogenic or fibrotic disorders, and to methods
CC   of determining the presence or absence of a pathological cell in a
CC   patient by detecting a nucleic acid at least 80% identical to those of
CC   the invention or by detecting a polypeptide of the invention. The
CC   invention also relates to expression vectors and host cells comprising a
CC   nucleic acid of the invention; antibodies which specifically bind a
CC   polypeptide of the invention; use of such antibodies for drug targeting;
CC   and methods of screening for modulators of activity or expression of the
CC   polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC   antibodies and methods are useful for diagnosing, prognosing and treating
CC   cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC   atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC   neovascularistaion syndromes, scarring and uterine fibroids. They may
CC   also be useful in wound healing and in contraception. The present
CC   sequence represents a nucleic acid sequence of the invention.
XX
SQ   Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:               0           Length:        4231
Score:                   6779.00     Matches:       1323
Percent Similarity:      99.9%       Conservative:  1
Best Local Similarity:   99.8%       Mismatches:    1
Query Match:             99.9%       Indels:        0
DB:                      11          Gaps:          0

US-09-976-858-42 (1-1325) x ADN39253 (1-4231)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315
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Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGAAAGAAATATGAA 1615

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1676 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1735

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1736 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1795

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1856 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2096 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2155

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2515

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2516 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2696 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2755

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2816 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
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Db       3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy       1321 PheGluThrAlaLeu 1325
              |||||||||||||||
Db       4076 TTCGAGACAGCACTG 4090

RESULT 12
ACL38944
ID   ACL38944 standard; cDNA; 4231 BP.
XX
AC   ACL38944;
XX
DT   24-MAR-2005  (first entry)
XX
DE   ABCC4 coding sequence, SEQ ID 1.
XX
KW   Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2005001092-A2.
XX
PD   06-JAN-2005.
XX
PF   19-MAY-2004; 2004WO-US015645.
XX
PR   20-MAY-2003; 2003US-0471729P.
XX
PA   (AMHP ) WYETH.
XX
PI   Be X,  Wei L,  Slonim DK,  Howes SH;
XX
DR   WPI; 2005-075568/08.
DR   P-PSDB; ABR99962.
XX
PT   Pharmaceutical composition comprising an agent capable of modulating an
PT   expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT   activated by the polypeptide or antibody, and a carrier, useful for
PT   treating cancer.
XX
PS   Claim 8; SEQ ID NO 1; 113pp; English.
XX
CC   The present invention relates to a novel pharmaceutical composition
CC   comprising: (a) an agent capable of modulating an expression level or
CC   protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC   ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC   (b) a carrier. The pharmaceutical composition may also comprise a
CC   polynucleotide capable of inhibiting or decreasing the expression of the
CC   CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC   invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC   FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC   pharmaceutical composition is useful for treating cancer, e.g. colon
CC   cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC   cancer, stomach cancer, and esophageal cancer. The present sequence is
CC   the coding sequence for one such CRTP. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0            Length:        4231
Score:                  6779.00      Matches:       1323
Percent Similarity:     99.9%        Conservative:  1
Best Local Similarity:  99.8%        Mismatches:    1
Query Match:            99.9%        Indels:        0
DB:                     14           Gaps:          0

US-09-976-858-42 (1-1325) x ACL38944 (1-4231)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||
Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715
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Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1676 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1735

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1736 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1795

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1856 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2096 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2155

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2515

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2516 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2696 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2755

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2816 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy       941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
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Db      2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy       961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy       981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
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Db      3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy      1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
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Db      3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy      1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
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Db      3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy      1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
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Db      3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy      1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355

Qy      1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Db      3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy      1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy      1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db      3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535

Qy      1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Qy      1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
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Db      3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy      1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
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Db      3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy      1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
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Db      3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy      1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy      1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
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Db      3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy      1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy      1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
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Db      3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy      1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy      1321 PheGluThrAlaLeu 1325
             |||||||||||||||
Db      4076 TTCGAGACAGCACTG 4090
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RESULT 13
AEA00097
ID   AEA00097 standard; cDNA; 4231 BP.
XX
AC   AEA00097;
XX
DT   28-JUL-2005  (first entry)
XX
DE   Human TAT131 cDNA SEQ ID NO:49.
XX
KW   ss; gene; tumor-associated antigen; cytostatic; breast tumor;
KW   endocrine disease; gynecology and obstetrics; neoplasm; colon tumor;
KW   gastrointestinal disease; rectal tumor; endometroid carcinoma;
KW   genitourinary disease; renal tumor; lung tumor; respiratory disease;
KW   ovary tumor; skin tumor; liver tumor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             116..4093
FT                   /*tag=  a
FT                   /product= "TAT131"
XX
PN   US2005106644-A1.
XX
PD   19-MAY-2005.
XX
PF   08-SEP-2004; 2004US-00936626.
XX
PR   20-JUN-2001; 2001US-0299500P.
PR   29-JUN-2001; 2001US-0301880P.
PR   18-SEP-2001; 2001US-0323268P.
PR   19-JUN-2002; 2002US-00177488.
PR   26-MAR-2004; 2004US-0557116P.
PR   04-AUG-2004; 2004US-0598899P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Cairns B,  Chen R,  Frantz G,  Hillan KJ,  Koeppen H,  Phillips HS;
PI   Polakis P,  Spencer SD,  Smith V,  Williams PM,  Wu TD,  Zhang Z;
PI   Sliwkowski M;
XX
DR   WPI; 2005-384304/39.
DR   P-PSDB; AEA00175.
XX
PT   Novel isolated antibody capable of binding to tumor-associated antigenic
PT   target polypeptide, useful for treating cell proliferative disorder e.g.
PT   cancer.
XX
PS   Claim 1; SEQ ID NO 49; 337pp; English.
XX
CC   The invention relates to a novel isolated antibody binding to a
CC   polypeptide having at least 80% sequence identity to a polypeptide having
CC   any one of 76 fully defined 182-910 amino acid tumor-associated antigenic
CC   target polypeptide (TAT) sequences (AEA00127-AEA00202) given in the
CC   specification, a polypeptide having any one of (AEA00127-AEA00202),
CC   lacking its associated signal peptide, or an extracellular domain of a
CC   polypeptide having any one of (AEA00127-AEA00202). The polypeptide is
CC   encoded by the nucleotide sequence having any one of (AEA00049-AEA00126).
CC   An antibody of the invention has cytostatic activity. The antibody is
CC   useful for inhibiting growth of a cell expressing TAT188, which involves
CC   contacting the cell with the antibody. The cell is a cancer cell chosen
CC   from breast, colon, rectum, endometrium, kidney, lung, ovary, skin and
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CC   liver cell. The cancer cell is a mammalian cell, preferably a human cell.
CC   The antibody is also is useful for detecting the level of TAT188
CC   polypeptide expressed in a test cell relative to a control cell, and for
CC   detecting the level of TAT188 polypeptide or a polypeptide having at
CC   least 80 % sequence identity to the TAT188 polypeptide sequence in a test
CC   cell relative to a control cell. The antibody is useful for treating a
CC   preventing a cell proliferative disorder associated with increased
CC   expression or activity of a polypeptide having at least 80 % identity to
CC   a TAT188 polypeptide sequence. The cell proliferative disorder is cancer.
CC   The method of the invention is useful for inhibiting the growth of a
CC   cancer cell. The present sequence encodes a polypeptide of the invention.
XX
SQ   Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              0           Length:         4231
Score:                  6779.00     Matches:        1323
Percent Similarity:     99.9%       Conservative:   1
Best Local Similarity:  99.8%       Mismatches:     1
Query Match:            99.9%       Indels:         0
DB:                     14          Gaps:           0

US-09-976-858-42 (1-1325) x AEA00097 (1-4231)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTGGGAAGTTGTTCTCATCA 895

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
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Db       1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1736 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1795

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Db       1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1856 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2096 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2155

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2515

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2516 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2696 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2755

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2816 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Db       3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Db       3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
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Db       3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy       1321 PheGluThrAlaLeu 1325
              |||||||||||||||
Db       4076 TTCGAGACAGCACTG 4090
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RESULT 14
AEA00617
ID   AEA00617 standard; cDNA; 4231 BP.
XX
AC   AEA00617;
XX
DT   28-JUL-2005  (first entry)
XX
DE   Human TAT131 cDNA sequence SeqID49.
XX
KW   antibody identification; tumor-associated antigen; cytostatic;
KW   RNA interference; gene therapy; cell death; cancer; breast tumor;
KW   colon tumor; rectal tumor; renal tumor; lung tumor; ovary tumor;
KW   skin tumor; liver tumor; gene; ss; TAT131.
XX
OS   Homo sapiens.
XX
PN   US2005107595-A1.
XX
PD   19-MAY-2005.
XX
PF   10-SEP-2004; 2004US-00938061.
XX
PR   20-JUN-2001; 2001US-0299500P.
PR   29-JUN-2001; 2001US-0301880P.
PR   18-SEP-2001; 2001US-0323268P.
PR   19-JUN-2002; 2002US-00177488.
PR   26-MAR-2004; 2004US-0557116P.
PR   04-AUG-2004; 2004US-0598899P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Cairns B,  Chen R,  Frantz G,  Hillan KJ,  Koeppen H,  Phillips HS;
PI   Polakis P,  Spencer SD,  Smith V,  Williams PM,  Wu TD,  Zhang Z;
PI   Sakanaka C,  Chuntharapai A,  Reed CJ;
XX
DR   WPI; 2005-371577/38.
DR   P-PSDB; AEA00695.
XX
PT   Novel isolated antibody e.g. anti-E16 or anti-TAT112 antibody that binds
PT   to tumor-associated antigenic target polypeptide, useful for diagnosing
PT   or treating cancer.
XX
PS   Claim 1; SEQ ID NO 49; 96pp; English.
XX
CC   This invention relates to a novel isolated antibody, for example anti-E16
CC   or anti-TAT112 antibody, that binds to a tumor-associated antigenic
CC   target polypeptide (TAT) and that lacks an associated signal peptide
CC   sequence. The invention may be useful for the development of compounds
CC   with a cytostatic activity acting as antagonists of the TAT188
CC   polypeptide or RNA interference whilst the disclosed sequences may be
CC   useful for gene therapy. The invention is useful for inducing the death
CC   of a cell (such as a cancer cell chosen from breast, colon, rectum,
CC   endometrium, kidney, lung, ovary, skin and liver) to which it binds,
CC   inhibiting proliferation or promoting cell death of a cell expressing
CC   TAT188. In addition, the invention may be useful for detecting the level
CC   of TAT188 polypeptide in a test cell relative to a control cell, or
CC   treating or preventing a cell proliferative disorder associated with
CC   increased expression of TAT188. The novel antibody of the invention is
CC   useful for inhibiting the growth of a cancer cell and may be useful for
CC   diagnosing or treating cancer. The present sequence is that of the human
CC   TAT131 cDNA which encodes a protein against which an antibody of the
CC   invention may be targeted.
XX
SQ   Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;

 Alignment Scores:
 Pred. No.:              0             Length:        4231
 Score:                  6779.00       Matches:       1323
 Percent Similarity:     99.9%         Conservative:  1
 Best Local Similarity:  99.8%         Mismatches:    1
 Query Match:            99.9%         Indels:        0
 DB:                     14            Gaps:          0
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US-09-976-858-42 (1-1325) x AEA00617 (1-4231)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy       361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy       381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy       401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy       421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy       441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy       461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy       481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615

Qy       501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy       521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1676 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1735

Qy       541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1736 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1795

Qy       561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855

Qy       581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1856 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915

Qy       601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy       621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy       641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095

Qy       661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2096 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2155

Qy       681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy       701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy       721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy       741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy       761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455

Qy       781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2515

Qy       801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2516 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575

Qy       821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy       841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695

Qy       861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2696 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2755

Qy       881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815

Qy       901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2816 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875

Qy       921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy       941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy       961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy       981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy      1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy      1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy      1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy      1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355
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Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy       1321 PheGluThrAlaLeu 1325
              |||||||||||||||
Db       4076 TTCGAGACAGCACTG 4090
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RESULT 15
ADR66822
ID   ADR66822 standard; DNA; 5832 BP.
XX
AC   ADR66822;
XX
DT   02-DEC-2004 (first entry)
XX
DE   Human prostatic carcinoma derived DNA SEQ ID 115 #4.
XX
KW   human; cytostatic; diagnosis; prostatic cancer;
KW   differential expression analysis; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004076614-A2.
XX
PD   10-SEP-2004.
XX
PF   22-FEB-2004; 2004WO-DE000433.
XX
PR   27-FEB-2003; 2003DE-01009985.
PR   14-MAY-2003; 2003DE-01022134.
XX
PA   (HINZ/) HINZMANN B.
PA   (DAHL/) DAHL E.
PA   (ROSE/) ROSENTHAL A.
PA   (HERM/) HERMANN K.
PA   (PILA/) PILARSKY C.
XX
PI   Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI   Schmitt A, Beckmann G, Bruemmendorf T, Kinnemann H, Roepcke S;
PI   Xinzhong L, Staub E;
XX
DR   WPI; 2004-653386/63.
XX
PT   New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT   useful for diagnosis, treatment and in screening for specific binding
PT   agents.
XX
PS   Claim 1; Page 1348-1349; 1607pp; German.
XX
CC   This invention describes novel cytostatic polynucleotide and polypeptide
CC   sequences which can be used in a method for diagnosing prostatic cancer
CC   or the risk of developing prostatic cancer. Diagnosis is based on
CC   determining over transcription or over expression of the sequences in
CC   prostatic tissue. Screening for inhibitors of the sequences or detection
CC   substances involves a binding assay, any compounds that bind are
CC   selected, optionally after deconvolution of mixtures. Detection of a
CC   predetermined minimum level of the reporter indicates the presence of
CC   tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC   short-interfering RNA or ribozymes; an organic molecule of molecular
CC   weight below 5000, preferably 300, that binds to the polypeptide; an
CC   aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC   polypeptide, preferably humanised or human; an anti-idiotype, non-human
CC   (monoclonal) antibody directed against Ab or any of the above derivatised
CC   with a reporter group, cell toxin, immunostimulatory molecules and/or
CC   radioisotope. The polynucleotides are identified in human prostatic
CC   cancer by differential expression analysis, using DNA microarrays,
CC   between normal and tumorous tissues, with (over)expression being detected
CC   by quantitative PCR. Analysis of prostatic cancer samples showed that
CC   CD24 was upregulated in many of them. Sections of tissue, isolated from
CC   prostatic cancer patients, or subjects at risk, were incubated
CC   sequentially with anti-human CD4 murine monoclonal antibodies;
CC   biotinylated second antibody; streptavidin-conjugated horseradish
CC   peroxidase and then diaminobenzidine as colour former (brown). The
CC   samples were counterstained with hemalum (blue). Malignant cells stained
CC   strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC   adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC   lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC   polynucleotide and polypeptide sequences used in the method of the
CC   invention.
XX
SQ   Sequence 5832 BP; 1660 A; 1175 C; 1306 G; 1691 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	5832
Score:	6779.00	Matches:	1323
Percent Similarity:	99.9%	Conservative:	1
Best Local Similarity:	99.8%	Mismatches:	1
Query Match:	99.9%	Indels:	0
DB:	13	Gaps:	0

US-09-976-858-42 (1-1325) x ADR66822 (1-5832)

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Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy           61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy           81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy          101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy          121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy          141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy          161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy          181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy          201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy          221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy          241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy          261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy          281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy          301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy          321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy          341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy          361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy          381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy          401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy          421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy          441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy          461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy          481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615

Qy          501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy          521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1676 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1735

Qy          541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1736 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1795

Qy          561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855

Qy          581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1856 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915

Qy          601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy          621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy          641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095

Qy          661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
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Db         2096 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2155

Qy          681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
                |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy          701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy          721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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Db         2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy          741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
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Db         2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy          761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455
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Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2515

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2516 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Db       2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
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Db       2696 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2755

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
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Db       2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Db       2816 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
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Db       2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
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Db       2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
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Db       2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
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Db       3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
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Db       3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Db       3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
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Db       3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||     |||
Db       3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
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Db       3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
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Db       3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
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Db       3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy       1321 PheGluThrAlaLeu 1325
              |||||||||||||||
Db       4076 TTCGAGACAGCACTG 4090
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Search completed: March 14, 2006, 08:36:53
Job time : 1773 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on:          March 14, 2006, 08:37:01 ; Search time 11315 Seconds
                                           (without alignments)
                                           5478.823 Million cell updates/sec

Title:           US-09-976-858-42
Perfect score:   6787
Sequence:        1 MLPVYQEVKPNPLQDANLCS..........MVTNTSNGQPSTLTIFETAL 1325

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:      82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US09976858/runat_13032006_170101_11806/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US09976858_@CGN_1_1_5315_@runat_13032006_170101_11806 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       EST:*
                 1:  gb_est1:*
                 2:  gb_est2:*
                 3:  gb_est3:*
                 4:  gb_htc:*
                 5:  gb_est4:*
                 6:  gb_est5:*
                 7:  gb_est6:*
                 8:  gb_est7:*
                 9:  gb_gss1:*
                 10:  gb_gss2:*
                 11:  gb_gss3:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5864	86.4	4594	4	AK052778	AK052778 Mus muscu
2	5553	81.8	3685	10	AY415506	AY415506 Homo sapi
3	4828	71.1	3679	10	AY415508	AY415508 Mus muscu
4	4395	64.8	3685	10	AY415507	AY415507 Pan trogl
5	2582	38.0	3208	4	AK032802	AK032802 Mus muscu
6	2263	33.3	5920	4	AK029876	AK029876 Mus muscu
7	2216.5	32.7	5899	4	CR749835	CR749835 Homo sapi
8	2144	31.6	4547	4	BC046560	BC046560 Mus muscu
9	2138	31.5	4953	10	CL969772	CL969772 OsIFCC018
10	2046.5	30.2	4638	11	DQ044660	DQ044660 Homo sapi
11	2043.5	30.1	4080	11	DQ038460	DQ038460 Homo sapi
12	1968.5	29.0	4185	10	AY407265	AY407265 Homo sapi
13	1957.5	28.8	4176	10	AY407267	AY407267 Mus muscu
14	1955	28.8	4483	10	CL957124	CL957124 OsJRUA001
15	1942.5	28.6	4425	10	CL970490	CL970490 OsIFCC019
16	1920.5	28.3	4185	10	AY407266	AY407266 Pan trogl
17	1888.5	27.8	4452	10	CL968077	CL968077 OsIFCC016
18	1883	27.7	4224	11	DQ049053	DQ049053 Homo sapi
19	1880	27.7	4425	10	CL963465	CL963465 OsIFCC009
20	1861	27.4	4773	11	DQ045352	DQ045352 Homo sapi
21	1835.5	27.0	1655	4	CNS0G6RE	CR704782 Tetraodon
22	1822.5	26.9	4080	11	DQ038461	DQ038461 Pan trogl
23	1817	26.8	4161	10	CL952237	CL952237 OsJRUA000
24	1813.5	26.7	3561	10	CL966129	CL966129 OsIFCC013
25	1797	26.5	4443	10	AY399795	AY399795 Homo sapi
26	1784.5	26.3	4686	10	CL969658	CL969658 OsIFCC018
27	1781	26.2	4149	11	DQ038456	DQ038456 Homo sapi
28	1726	25.4	4542	10	AY412332	AY412332 Homo sapi
29	1706.5	25.1	3588	10	CL964834	CL964834 OsIFCC011
30	1697	25.0	4529	10	AY412334	AY412334 Mus muscu
31	1688	24.9	3975	10	AY399797	AY399797 Mus muscu
32	1682.5	24.8	4638	11	DQ044661	DQ044661 Pan trogl
33	1661.5	24.5	1493	4	CNS0FQBA	CR683466 Tetraodon
34	1657	24.4	3561	10	CL979509	CL979509 OsIFCC033
35	1624	23.9	3597	10	CL966131	CL966131 OsIFCC013
36	1536	22.6	2516	4	AK049174	AK049174 Mus muscu
37	1520	22.4	4773	11	DQ045353	DQ045353 Pan trogl
38	1514.5	22.3	2397	10	CL958547	CL958547 OsIFCC001
39	1507	22.2	4905	10	CL963549	CL963549 OsIFCC009
40	1501	22.1	3361	4	AK083916	AK083916 Mus muscu
41	1499.5	22.1	3174	11	DQ050048	DQ050048 Homo sapi
42	1455	21.4	4242	10	AY399796	AY399796 Pan trogl
43	1317	19.4	1195	8	DN698293	DN698293 CLJ16-G03
44	1250.5	18.4	4460	11	DQ030756	DQ030756 Homo sapi
45	1250	18.4	1084	3	BM462073	BM462073 AGENCOURT

ALIGNMENTS

```
RESULT 1
AK052778
LOCUS       AK052778                4594 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched
            library, clone:D630049P08 product:ATP-binding cassette, sub-family
            C (CFTR/MRP), member 4 homolog (Human), full insert sequence.
ACCESSION   AK052778
VERSION     AK052778.1  GI:26095372
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
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            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 4594)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1..4594
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:D630049P08"
                     /db_xref="taxon:10090"
                     /clone="D630049P08"
                     /tissue_type="kidney"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="0 day neonate"
     misc_feature    1..4594
                     /note="ATP-binding cassette, sub-family C (CFTR/MRP),
                     member 4 homolog (Human) (SWISSPROT|O15439, evidence:
                     FASTY, 86.9%ID, 98.1%length, match=3904)"
ORIGIN

Alignment Scores:
Pred. No.:               0               Length:          4594
Score:                   5864.00         Matches:         1131
Percent Similarity:      92.5%           Conservative:    74
Best Local Similarity:   86.9%           Mismatches:      96
Query Match:             86.4%           Indels:          1
DB:                      4               Gaps:            0

US-09-976-858-42 (1-1325) x AK052778 (1-4594)
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Qy     25 TrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGluGluAspAspMet 44
          ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db    166 TGGTGGCTCAACCCGCTGTTTAAAACTGGTCATAAGCGGAGACTGGAAGAAGATGACATG 225

Qy     45 TyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheTrp 64
          :::||||||||||||||||||||||||:::|||||||||||||||||||||   :::|||
Db    226 TTCTCAGTGCTTCCAGAAGATCGCTCAAAGCACCTCGGAGAGGAGCTTCAACGGTACTGG 285

Qy     65 AspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArgAlaIle 84
          |||||||||:::|||||||||:::   |||::::::|||||||||||||||:::||||||
Db    286 GATAAAGAACTTCTGCGAGCCAAGAAGGACTCGAGGAAGCCCTCCTTAACAAAGGCAATC 345

Qy     85 IleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGluGluSer 104
          |||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||   
Db    346 ATAAAGTGTTACTGGAAGTCTTACCTGATTTTGGGAATTTTTACGTTAATTGAGGAGGGC 405

Qy    105 AlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAsp 124
             :::|||:::||||||:::||||||||||||||||||   |||||||||   ||||||
Db    406 ACTCGAGTAGTTCAGCCCTTATTTTTAGGGAAAATTATTGAATATTTTGAGAAGTATGAC 465

Qy    125 ProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCys 144
          |||   |||||||||||||||:::|||||||||   ||||||   ||||||:::   |||
Db    466 CCCGACGACTCGGTGGCTTTGCATACAGCTTATGGCTACGCAGCAGTGCTGTCCATGTGC 525

Qy    145 ThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCysAlaGlyMet 164
          |||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db    526 ACGCTCATCCTGGCCATACTACATCATTTGTACTTGTACCACGTGCAGTGCGCCGGGATG 585

Qy    165 ArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsnMet 184
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||   
Db    586 AGGCTGCGGGTTGCCATGTGCCACATGATTTACCGGAAGGCACTCCGGTTAAGTAACTCG 645

Qy    185 AlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsnLys 204
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    646 GCCATGGGGAAGACAACCACAGGCCAGATAGTTAACCTGCTGTCCAACGACGTGAACAAA 705

Qy    205 PheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIleAla 224
          |||||||||||||||:::|||||||||||||||||||||||||||||||||   ||||||
Db    706 TTCGACCAAGTGACAATCTTCTTGCACTTTCTGTGGGCAGGGCCGCTGCAGCCCATCGCG 765

Qy    225 ValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaValLeu 244
          ||||||   |||||||||:::|||||||||||||||||||||||||||:::|||||||||
Db    766 GTAACCGTCCTCCTCTGGGTGGAGATAGGAATCTCCTGCCTGGCGGGCTTGGCCGTTCTG 825

Qy    245 IleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLys 264
          :::||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db    826 GTTATTCTTCTGCCTCTGCAAAGCTGCATCGGGAAGCTGTTCTCGTCACTGCGGAGTAAA 885

Qy    265 ThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIleArg 284
          ||||||   |||||||||||||||||||||||||||||||||||||||||||||:::|||
Db    886 ACTGCGGCTTTCACGGATGCCAGGATCCGGACCATGAATGAAGTCATAACAGGCATGAGG 945

Qy    285 IleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArgLys 304
          |||||||||||||||||||||||||||||||||::::::||||||   ||||||||||||
Db    946 ATAATAAAGATGTATGCGTGGGAGAAATCGTTTGCTGACCTCATTGCCAATCTGAGAAAG 1005

Qy    305 LysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAlaSerPhe 324
          |||||||||||||||||||||   ||||||   |||||||||||||||:::|||||||||
Db   1006 AAGGAGATTTCCAAGATTCTGGGCAGCTCCTACCTCAGAGGGATGAACATGGCGTCGTTT 1065

Qy    325 PheSerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeuGlySer 344
          |||   |||:::|||:::|||:::|||||||||||||||:::|||||||||||||||:::
Db   1066 TTCATCGCAAACAAAGTCATCCTGTTCGTGACCTTCACTAGCTACGTGCTGCTTGGCAAT 1125

Qy    345 ValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValArgLeuThr 364
             ||||||||||||   ||||||||||||:::|||||||||||||||||||||||||||
Db   1126 GAGATTACAGCTAGCCACGTGTTTGTGGCCATGACTCTGTACGGTGCCGTTCGGTTGACA 1185

Qy    365 ValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIleArg 384
          |||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db   1186 GTCACCCTCTTCTTCCCGTCAGCCATTGAGAGAGGGTCAGAGGCCATCGTCAGCATTCGG 1245
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Qy    385 ArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuProSer 404
Db   1246 AGGATCAAGAACTTTCTGTTACTCGATGAACTACCACAGCGCAAAGCCCATGTACCATCT 1305

Qy    405 AspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGlu 424
Db   1306 GATGGCAAAGCCATTGTCCACGTGCAAGATTTCACCGCTTTCTGGGACAAGGCACTAGAC 1365

Qy    425 ThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValVal 444
Db   1366 AGTCCAACCCTGCAAGGTCTTTCCTTTATTGCCAGGCCTGGTGAGTTGTTAGCCGTGGTT 1425

Qy    445 GlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaPro 464
Db   1426 GGCCCAGTTGGAGCAGGCAAGTCGTCGCTGTTGAGCGCAGTGCTGGGTGAGCTGCCTCCT 1485

Qy    465 SerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpVal 484
Db   1486 GCCAGCGGGCTGGTCAGCGTGCACGGGAGGATCGCCTACGTTTCTCAGCAGCCCTGGGTG 1545

Qy    485 PheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyr 504
Db   1546 TTCTCGGGCACCGTGAGGAGCAATATTTTATTTGGGAAGAAATATGAGAAGGAGCGATAT 1605

Qy    505 GluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAsp 524
Db   1606 GAGAAAGTGATCAAGGCCTGTGCTCTGAAGAAGGACCTGCAGCTTCTGGAGGACGGGGAT 1665

Qy    525 LeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsn 544
Db   1666 CTGACGGTTATAGGAGACCGGGGAGCCACGCTGAGTGGAGGCCAGAAAGCTCGGGTGAAC 1725

Qy    545 LeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAla 564
Db   1726 CTGGCACGGGCCGTCTACCAGGACGCCGACATCTACCTCCTTGATGATCCGCTCAGCGCT 1785

Qy    565 ValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeuHisGlu 584
Db   1786 GTCGATGCAGAAGTGGGCAAGCACCTGTTCCAACTGTGTATCTGTCAGGCGTTGCACGAG 1845

Qy    585 LysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeu 604
Db   1846 AAGATCACCATTTTAGTGACTCACCAGTTACAGTACCTCAAAGCTGCAAGCCACATCCTC 1905

Qy    605 IleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGly 624
Db   1906 ATACTCAAAGATGGTGAGATGGTGCAGAAGGGGACTTACACGGAGTTTCTGAAATCTGGT 1965

Qy    625 IleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProProValPro 644
Db   1966 GTAGATTTTGGCTCCCTGTTAAAGAAAGAAAACGAGGAAGCAGAGCCCTCCACAGCCCCA 2025

Qy    645 GlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGlnGlnSer 664
Db   2026 GGAACCCCGACACTCAGGAAACGAACCTTCTCCGAGGCCTCAATTTGGTCTCAGCAGTCA 2085

Qy    665 SerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnValProVal 684
Db   2086 TCCAGACCCTCGTTGAAAGACGGGGCCCCAGAGGGCCAAGACGCAGAGAACACGCAGGCA 2145

Qy    685 ThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLysAsnTyr 704
Db   2146 GTGCAACCCGAGGAGAGCCGTTCGGAAGGGAGAATCGGCTTCAAGGCCTACAAGAATTAC 2205

Qy    705 PheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAlaAla 724
Db   2206 TTCTCGGCGGGCGCATCCTGGTTCTTCATCATTTTCCTTGTGCTGCTTAACATGGTGGGC 2265

Qy    725 GlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMet 744
Db   2266 CAGGTTTTCTATGTTCTTCAGGACTGGTGGCTTTCCCACTGGGCGAACAAGCAAGGTGCA 2325

Qy    745 LeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsnTrpTyr 764

Db   2326 CTGAACAACACCAGAAATGCGAATGGAAATATAACGGAGACCCTAGACCTCAGCTGGTAC 2385

Qy    765 LeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeu 784
Db   2386 TTAGGAATTTACGCAGGTCTAACTGCGGTCACCGTCCTTTTGGCATAGCGAGATCCCTA 2445

Qy    785 LeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGluSer 804
Db   2446 CTGGTGTTCTATATCCTTGTGAACGCTTCCCAGACTTTGCACAACAGGATGTTTGAGTCC 2505

Qy    805 IleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArg 824
Db   2506 ATACTGAAGGCTCCCGTGTTGTTCTTCGACAGAAATCCAATCGGGAGGATTTTAAATCGT 2565

Qy    825 PheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIle 844
Db   2566 TTCTCCAAAGACATCGGACACATGGATGATTTGCTTCCCCTGACGTTCCTGGACTTCATC 2625

Qy    845 GlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaValIleProTrpIle 864
Db   2626 CAGACGTTGCTCCTCGTCGTAAGTGTGATCGCTGTGGCCGCGGCCGTGATCCCTTGGATC 2685

Qy    865 AlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGlu 884
Db   2686 CTCATACCATTGGTTCCGCTCTCAGTCGTCTTCCTGGTTCTTCGGAGATACTTCTTAGAG 2745

Qy    885 ThrSerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSerHisLeu 904
Db   2746 ACGTCACGGGATGTCAAGCGCCTGGAATCCACAACACGGAGCCCGGTATTCTCCCATTTA 2805

Qy    905 SerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArgCysGln 924
Db   2806 TCGTCCTCCCTCCAGGGACTCTGGACCATCCGGGCTTACAAAGCTGAGGAGAGGTGTCAG 2865

Qy    925 GluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThr 944
Db   2866 GAGCTGTTTGATGCACACCAGGACTTGCATTCAGAGGCTTGGTTCTTGTTCCTGACGACA 2925

Qy    945 SerArgTrp-PheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAl 964
Db   2926 TCGAGATGGTTTCGCTGTGCGTCTGGACGCCATCTGCGCCATCTTTGTAATCGTCGTTGC 2985

Qy    964 aPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSe 984
Db   2986 CTTCGGGTCCCTTGTTCTGGCGAAGACTTTGAATGCTGGGCAGGTTGGCCTGGCCTTGTC 3045

Qy    984 rTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGluValGl 1004
Db   3046 CTACGCCCTCACACTCATGGGGATGTTCCAGTGGTCTGTGCGACAGAGCGCCGAAGTAGA 3105

Qy   1004 uAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGluAlaPr 1024
Db   3106 GAATATGATGATTTCAGTGGAGAGAGTGATTGAGTACACGGACCTAGAGAAGGAGGCGCC 3165

Qy   1024 oTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyValIleIlePheAs 1044
Db   3166 TTGGGAGTGCAAGAAGCGCCCACCCCCAGGCTGGCCCCACGAGGGAGTCATCGTCTTCGA 3225

Qy   1044 pAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAlaLe 1064
Db   3226 CAATGTGAACTTCACCTACAGCTTAGATGGGCCTCTGGTTCTGAAGCACCTGACTGCGCT 3285

Qy   1064 uIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLe 1084
Db   3286 CATCAAGTCCAGGGAAAAGGTTGGAATTGTGGGCAGAACCGGAGCTGGGAAAAGCTCCCT 3345

Qy   1084 uIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIleAspLysIleLe 1104
Db   3346 CATCTCGGCCCTCTTCAGGCTGTCAGAACCCGAGGGGAAAATCTGGATCGATAAGATCTT 3405

Qy   1104 uThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGluPr 1124
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Db        3406 GACAACCGAAATTGGGCTTCACGACTTAAGGAAGAAAATGTCAATCATACCACAGGAACC 3465

Qy        1124 oValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThrAspGl 1144
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Db        3466 TGTTCTGTTCACTGGAACCATGAGGAAAAACCTGGACCCCTTCAATGAGCACACGGACGA 3525

Qy        1144 uGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGl 1164
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Db        3526 GGAGCTGTGGAGGGCCTTGGAGGAGGTACAACTTAAAGAGGCCATTGAAGATCTTCCTGG 3585

Qy        1164 yLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGlnArgGlnLe 1184
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Db        3586 AAAAATGGATACTGAATTAGCAGAATCTGGATCCAATTTCAGTGTTGGACAGAGACAGTT 3645

Qy        1184 uValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAlaTh 1204
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Db        3646 AGTGTGCCTTGCAAGGGCCATTCTAAAGAATAACCGAATACTGATCATTGATGAAGCAAC 3705

Qy        1204 rAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPheAl 1224
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Db        3706 TGCAAATGTGGACCCAAGAACGGATGAGTTAATACAACAGAAGATCCGGGAGAAGTTTGC 3765

Qy        1224 aHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLysIl 1244
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Db        3766 CCAGTGCACAGTGCTCACCATTGCTCACAGACTGAACACCATCATTGACAGTGACAAGAT 3825

Qy        1244 eMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGlnAs 1264
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Db        3826 AATGGTTTTGGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTCTTGCTGCAGAA 3885

Qy        1264 nLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGluAlaAlaAlaLe 1284
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Db        3886 TCCAGAGAGCCTCTTTTACAAGATGGTTCAGCAACTGGGCAAGGGCGAAGCCGCTGCCCT 3945

Qy        1284 uThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIleGlyHisThrAs 1304
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Db        3946 CACCGAAACAGCAAAACAGGTATACTTCAGACGGAATTACCCACATATTACATTCACCAG 4005

Qy        1304 pHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIlePheGluThrAl 1324
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Qy        1324 aLeu 1325
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Db        4066 ATTG 4069
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RESULT 2
AY415506

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LOCUS       AY415506                3685 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Homo sapiens ABCC4 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY415506
VERSION     AY415506.1  GI:39771465
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 3685)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 3685)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1..>3685
                     /gene="ABCC4"
                     /locus_tag="HCM5580"
ORIGIN

Alignment Scores:
Pred. No.:              0               Length:         3685
Score:                  5553.00         Matches:        1107
Percent Similarity:     90.1%           Conservative:   0
Best Local Similarity:  90.1%           Mismatches:     121
Query Match:            81.8%           Indels:         0
DB:                     10              Gaps:           0

US-09-976-858-42 (1-1325) x AY415506 (1-3685)

Qy          63 PheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArg 82
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 TTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGA 61

Qy          83 AlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGlu 102
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 GCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTGGGAATTTTTACGTTAATTGAG 121

Qy         103 GluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsn 122
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         122 NNNNNTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTTGAAAAT 181

Qy         123 TyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThr 142
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         182 TATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTGCTGACT 241

Qy         143 PheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCysAla 162
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         242 TTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAGTGTGCT 301

Qy         163 GlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSer 182
               ||||||||||||||||||||||||||||||||||||||||||||||
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Qy         183 AsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspVal 202

Db         362 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 421

Qy         203 AsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAla 222
                              ||||||||||||||||||||||||||||||||||||||||||||||
Db         422 NNNNNNNNNNNNNNNGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTGCAGGCG 481

Qy         223 IleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAla 242
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Qy         243 ValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArg 262
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Db         542 GTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCACTGAGG 601

Qy         263 SerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGly 282
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         602 AGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGGT 661

Qy         283 IleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeu 302
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         662 ATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTTG 721
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Qy        303 ArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAla 322
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Db        722 AGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGAGGGATGAATTTGGCT 781

Qy        323 SerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeu 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 TCATTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTGCTCCTC 841

Qy        343 GlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValArg 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 GGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCTGTGCGG 901

Qy        363 LeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSer 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 CTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATCGTCAGC 961

Qy        383 IleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeu 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 ATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGTCAGCTG 1021

Qy        403 ProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAspLysAla 422
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Db       1022 CCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCA 1081

Qy        423 SerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAla 442
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Db       1082 TCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGCT 1141

Qy        443 ValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeu 462
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Db       1142 GTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATTG 1201

Qy        463 AlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnPro 482
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Db       1202 GCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAGCAGCCC 1261

Qy        483 TrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGlu 502
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Db       1262 TGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAAGGAA 1321

Qy        503 ArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAsp 522
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Db       1322 CGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGAT 1381

Qy        523 GlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArg 542
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Db       1382 GGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAAGCACGG 1441

Qy        543 ValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeu 562
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Db       1442 GTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTC 1501

Qy        563 SerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeu 582
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Db       1502 AGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAATTTTG 1561

Qy        583 HisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGln 602
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Db       1562 CATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAG 1621

Qy        603 IleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLys 622
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Db       1622 ATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAA 1681

Qy        623 SerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProPro 642
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Db       1682 TCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCA 1741

Qy        643 ValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGln 662
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Db       1742 GTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAA 1801

Qy        663 GlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnVal 682
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Db       1802 CAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTC 1861

Qy        683 ProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLys 702
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Db       1862 CCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAG 1921

Qy        703 AsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThr 722
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Qy        723 AlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGln 742
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Qy        743 SerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsn 762
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Db       2042 AGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAAC 2101

Qy        763 TrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArg 782
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Db       2102 TGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAGA 2161

Qy        783 SerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPhe 802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2162 TCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAAATGTTT 2221

Qy        803 GluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeu 822
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Qy        823 AsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAsp 842
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Db       2282 AATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGAT 2341

Qy        843 PheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaValIlePro 862
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Db       2342 TTCATCCAGNCATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTGATTCCT 2401

Qy        863 TrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPhe 882
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Db       2462 TTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCC 2521

Qy        903 HisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArg 922
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Qy        923 CysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeu 942
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Qy        943 ThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIle 962
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Db       2642 ACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTCATCATC 2701

Qy        963 ValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAla 982
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Db       2702 GTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGTTTGGCA 2761

Qy        983 LeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGlu 1002
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Db       2762 CTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGTGCTGAA 2821

Qy       1003 ValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGlu 1022
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Db       2822 GTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAAAAAGAA 2881

Qy       1023 AlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyValIleIle 1042
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Db       2882 GCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTGATAATC 2941

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Qy       1063 AlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSer 1082
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Qy       1103 IleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGln 1122

Db       3122 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3181

Qy       1123 GluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThr 1142
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Db       3182 GAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAGCACACG 3241

Qy       1143 AspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeu 1162
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Qy       1163 ProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGlnArg 1182
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Db       3302 CCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGA 3361

Qy       1183 GlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGlu 1202
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Db       3362 CAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATTGATGAA 3421

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Db       3422 GCGACGGCAAATGTGGATCCAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3481

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Qy       1243 LysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeu 1262
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Db       3542 NNNNNNNNNGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTTTTGCTG 3601

Qy       1263 GlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGluAlaAla 1282
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RESULT 3
AY415508

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LOCUS       AY415508                3679 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Mus musculus ABCC4 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY415508
VERSION     AY415508.1  GI:39771467
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3679)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 3679)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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                     /db_xref="taxon:10090"
     gene            <1..>3679
                     /gene="ABCC4"
                     /locus_tag="HCM5580"
ORIGIN

Alignment Scores:
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Score:                  4828.00        Matches:       954
Percent Similarity:     83.3%          Conservative:  70
Best Local Similarity:  77.6%          Mismatches:    202
Query Match:            71.1%          Indels:        4
DB:                     10             Gaps:          1

US-09-976-858-42 (1-1325) x AY415508 (1-3679)

Qy         63 PheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArg 82
              :::||||||||||||:::|||||||||:::      |||::::::||||||||||||:::
Db          2 TACTGGGATAAAGAACTTCTGCGAGCCAAGAAGGACTCGAGGAAGCCCTCCTTAACAAAG 61

Qy         83 AlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGlu 102
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Db         62 GCAATCATAAAGTGTTACTGGAAGTCTTACCTGATTTTGGGAATTTTTACGTTAATTGAG 121

Qy        103 GluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsn 122
              |||      :::|||:::||||||:::||||||||||||||||||   |||||||||
Db        122 GAGGGCACTCGAGTAGTTCAGCCCTTATTTTTAGGGAAAATTATTGAATATTTTGAGAAG 181

Qy        123 TyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThr 142
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Db        182 TATGACCCCGACGACTCGGTGGCTTTGCATACAGCTTATGGCTACGCAGCAGTGCTGTCC 241

Qy        143 PheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCysAla 162
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Db        242 ATGTGCACGCTCATCCTGGCCATACTACATCATTTGTACTTCTACCACGTGCAGTGCGCC 301

Qy        163 GlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAla-LeuArgLeuSe 182
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Db        302 GGGATGAGGCTGCGGGTTGCCATGTGCCACATGATTTAC------CNNNNNNNNNNNNNN 355

Qy        182 rAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspVa 202

Db        356 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 415

Qy        202 lAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAl 222
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Qy        222 aIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAl 242
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Qy        242 aValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuAr 262
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Qy        262 gSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGl 282
Db        596 GAGTAAAACTGCGGCTTTCACGGATGCCAGGATCCGGACCATGAATGAAGTCATAACAGG 655
Qy        282 yIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLe 302
Db        656 CATGAGGATAATAAAGATGTATGCGTGGGAGAAATCGTTTGCTGACCTCATTGCCAATCT 715
Qy        302 uArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAl 322
Db        716 GAGAAAGAAGGAGATTTCCAAGATTCTGGGCAGCTCCTACCTCAGAGGGATGAACATGGC 775
Qy        322 aSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLe 342
Db        776 GTCGTTTTTCATCGCAAACAAAGTCATCCTGTTCGTGACCTTCACTAGCTACGTGCTGCT 835
Qy        342 uGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValAr 362
Db        836 TGGCAATGAGATTACAGCTAGCCACGTGTTTGTGGCCATGACTCTGTACGGTGCCGTTCG 895
Qy        362 gLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSe 382
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Qy        382 rIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLe 402
Db        956 CATTCGGAGGATCAAGAACTTTCTGTTACTCGATGAACTACCACAGCGCAAAGCCCATGT 1015
Qy        402 uProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAspLysAl 422
Db       1016 ACCATCTGATGGCAAAGCCATTGTCCACGTGCAAGATTTCACCGCTTTCTGGGACAAGGC 1075
Qy        422 aSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAl 442
Db       1076 ACTAGACAGTCCAACCCTGCAAGGTCTTTCCTTTATTGCCAGACCTGGTGAGTTGTTAGC 1135
Qy        442 aValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLe 462
Db       1136 CGTGGTTGGCCCAGTTGGAGCAGGCAAGTCGTCGCTGTTGAGCGCAGTGCTGGGTGAGCT 1195
Qy        462 uAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnPr 482
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Qy        502 uArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAs 522
Db       1316 GCGATATGAGAAAGTGATCAAGGCCTGTGCTCTGAAGAAGGACCTGCAGCTTCTGGAGGA 1375
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Qy        562 uSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLe 582
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Qy        582 uHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGl 602
Db       1556 GCACGAGAAGATCACCATTTTAGTGACTCACCAGTTACAGTACCTCAAAGCTGCAAGCCA 1615
Qy        602 nIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLy 622
Db       1616 CATCCTCATACTCAAAGATGGTGAGATGGTGCAGAAGGGGACTTACACGGAGTTTCTGAA 1675
Qy        622 sSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProPr 642
Db       1676 ATCTGGTGTAGATTTTGGCTCCCTGTTAAAGAAAGAAAACGAGGAAGCAGAGCCCTCCAC 1735
Qy        642 oValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGl 662
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Qy        682 lProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLy 702
Db       1856 GCAGGCAGTGCAACCCGAGGAGAGCCGTTCGGAAGGGAGAATCGGCTTCAAGGCCTACAA 1915
Qy        702 sAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnTh 722
Db       1916 GAATTACTTCTCGGCGGGCGCATCCTGGTTCTTCATCATTTTCCTTGTGCTGCTTAACAT 1975
Qy        722 rAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGl 742
Db       1976 GGTGGGCCAGGTTTTCTATGTTCTTCAGGACTGGTGGCTTTCCCACTGGGCGAACAAGCA 2035
Qy        742 nSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAs 762
Db       2036 AGGTGCACTGAACAACACCAGAAATGCGAATGGAAATATAACGGAGACCCTAGACCTCAG 2095
Qy        762 nTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaAr 782
Db       2096 CTGGTACTTAGGAATTTACGCAGGTCTAACTGCGGTCACCGTCCTTTTTGGCATAGCGAG 2155
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Qy        802 eGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLe 822
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Qy        862 oTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPh 882
Db       2396 TTGGATCCTCATACCATTGGTTCCGCTCTCAGTCGTCTTCCTGGTTCTTCGGAGATACTT 2455
Qy        882 eLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSe 902
Db       2456 CTTAGAGACGTCACGGGATGTCAAGCGCCTGGAATCCAC-ACACGGAGCCCGGTATTCTC 2514
Qy        902 rHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluAr 922
Db       2515 CCATTTATCGTCCTCCCTCCAGGGACTCTGGACCATCCGGGCTTACAAAGCTGAGGAGAG 2574
Qy        922 gCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLe 942
Db       2575 GTGTCAGGAGCTGTTTGATGCACACCAGGACTTGCATTCAGAGGCTTGGTTCTTGTTCCT 2634
Qy        942 uThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIl 962
Db       2635 GACGACATCGAGATGGTTCGCTGTGCGTCTGGACGCCATCTGCGCCATCTTTGTCATCGT 2694
Qy        962 eValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAl 982
Db       2695 CGTTGCCTTCGGGTCCCTTGTTCTGGCGAAGACTTTGAATGCTGGGCAGGTTGGCCTGGC 2754
Qy        982 aLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGl 1002
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Db       2755 CTTGTCCTACGCCCTCACACTCATGGGGATGTTCCAGTGGTCTGTGCGACAGAGCGCCGA 2814

Qy       1002 uValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGl 1022
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Db       2815 AGTAGAGAATATGATGATTTCAGTGGAGAGAGTGATTGAGTACACGGACCTAGAGAAGGA 2874

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Db       2995 TGCGCTCATCAAGTCCAGGGAAAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3054

Qy       1082 rSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIleAspLy 1102

Db       3055 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3114

Qy       1102 sIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGl 1122

Db       3115 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3174

Qy       1122 nGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisTh 1142
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Db       3175 NGAACCTGTTCTGTTCACTGGAACCATGAGGAAAAACCTGGACCCCTTCAATGAGCACAC 3234

Qy       1142 rAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLe 1162
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Db       3235 GGACGAGGAGCTGTGGAGGGCCTTGGAGGAGGTACAACTTAAAGAGGCCATTGAAGATCT 3294

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Db       3355 ACAGTTAGTGTGCCTTGCAAGGGCCATTCTAAAGAATAACCGAATACTGATCATTGATGA 3414

Qy       1202 uAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLy 1222
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Db       3415 AGCAACTGCAAATGTGGACCCAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3474

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Qy       1242 pLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLe 1262
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Db       3535 NNNNNNNNNGTTTTGGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTCTTGCT 3594

Qy       1262 uGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGluAlaAl 1282
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Db       3595 GCAGAATCCAGAGAGCCTCTTTTACAAGATGGTTCAGCAACTGGGCAAGGGCGAAGCCGC 3654

Qy       1282 aAlaLeuThrGluThrAlaLysGln 1290
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Db       3655 TGCCCTCACCGAAACAGCAAAACAG 3679

RESULT 4
AY415507
LOCUS       AY415507               3685 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Pan troglodytes ABCC4 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY415507
VERSION     AY415507.1  GI:39771466
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 3685)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 3685)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1..>3685
                     /gene="ABCC4"
                     /locus_tag="HCM5580"
ORIGIN

Alignment Scores:
Pred. No.:               0           Length:         3685
Score:                   4395.00     Matches:        908
Percent Similarity:      73.9%       Conservative:   0
Best Local Similarity:   73.9%       Mismatches:     320
Query Match:             64.8%       Indels:         0
DB:                      10          Gaps:           0

US-09-976-858-42 (1-1325) x AY415507 (1-3685)

Qy         63 PheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArg 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGA 61

Qy         83 AlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGlu 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGCATTTTTACGTTAATTGAG 121

Qy        103 GluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsn 122

Db        122 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 181

Qy        123 TyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThr 142

Db        182 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 241

Qy        143 PheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCysAla 162

Db        242 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 301

Qy        163 GlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSer 182

Db        302 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 361

Qy        183 AsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspVal 202

Db        362 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 421

Qy        203 AsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAla 222
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Db        422 NNNNNNNNNNNNNNNGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTGCAGGCG 481
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Qy     223 IleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAla 242
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Qy     243 ValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArg 262
Db     542 GTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCACTGAGG 601

Qy     263 SerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGly 282
Db     602 AGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGGT 661

Qy     283 IleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeu 302
Db     662 ATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTTG 721

Qy     303 ArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAla 322
Db     722 AGAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 781

Qy     323 SerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeu 342
Db     782 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 841

Qy     343 GlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValArg 362
Db     842 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 901

Qy     363 LeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSer 382
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Qy     383 IleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeu 402
Db     962 NNNNNNNNNNNNNNNACCTTTTGCTACTTGATGAGATATCACAGCGCAACCGTCAGCTG 1021

Qy     403 ProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAspLysAla 422
Db    1022 CCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCA 1081

Qy     423 SerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAla 442
Db    1082 TCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGCT 1141

Qy     443 ValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeu 462
Db    1142 GTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATTG 1201

Qy     463 AlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnPro 482
Db    1202 GCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAGCAGCCC 1261

Qy     483 TrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGlu 502
Db    1262 TGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAAGGAA 1321

Qy     503 ArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAsp 522
Db    1322 CGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGNNNNNNNNNNNNNNNNNNNNN 1381

Qy     523 GlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArg 542
Db    1382 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1441

Qy     543 ValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeu 562
Db    1442 NNNNNNNNNNNNNNAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTC 1501

Qy     563 SerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeu 582
Db    1502 AGTGNNNNNNNNTGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAACTTTG 1561

Qy     583 HisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGln 602
Db    1562 CATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAG 1621

Qy     603 IleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLys 622
Db    1622 ATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAA 1681

Qy     623 SerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProPro 642
Db    1682 TCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGACAACGAGGAAAGTGAACAACCTCCA 1741

Qy     643 ValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGln 662
Db    1742 GTTCCAGGAACTCCCACACTGAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAA 1801

Qy     663 GlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnVal 682
Db    1802 CAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTC 1861

Qy     683 ProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLys 702
Db    1862 CCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAG 1921

Qy     703 AsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThr 722
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Qy     723 AlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGln 742
Db    1982 GCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAACAA 2041

Qy     743 SerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsn 762
Db    2042 AGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAAC 2101

Qy     763 TrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArg 782
Db    2102 TGGTACTTAGGAATTTATTCAGGTTTAACAGTAGCTACCGTTCTTTTCGGCATAGCAAGA 2161

Qy     783 SerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPhe 802
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Qy     803 GluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeu 822
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Qy     823 AsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAsp 842
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Qy     883 LeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSer 902
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Qy     903 HisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArg 922
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Qy     923 CysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeu 942
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Qy     943 ThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIle 962
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Db       2642 ACAACGTCCCGCTGGTTCGCTGTCCGTCTGGATGCCATCTGTGCCATGTTTGTCATCATC 2701

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Db       2882 GCACCTTGGGAATATCAGAAACGCCCACCACCGGCCTGGCCCCATGAAGGAGTGATAATC 2941

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Qy       1063 AlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSer 1082
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Qy       1083 SerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIleAspLys 1102

Db       3062 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3121

Qy       1103 IleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGln 1122

Db       3122 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3181

Qy       1123 GluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThr 1142
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Qy       1243 LysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeu 1262
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Db       3542 NNNNNNNNNGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTTTTGCTG 3601

Qy       1263 GlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGluAlaAla 1282
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RESULT 5
AK032802
LOCUS       AK032802                3208 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 12 days embryo male wolffian duct includes surrounding
            region cDNA, RIKEN full-length enriched library, clone:6720455A17
            product:ATP-binding cassette, sub-family C (CFTR/MRP), member 4
            homolog (Human), full insert sequence.
ACCESSION   AK032802
VERSION     AK032802.1  GI:26083045
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3208)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
```

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            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
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                     /dev_stage="12 days embryo"
     misc_feature    1..3208
                     /note="ATP-binding cassette, sub-family C (CFTR/MRP),
                     member 4 homolog (Human) (SWISSPROT|O15439, evidence:
                     FASTY, 86.9%ID, 98.1%length, match=3904)"
ORIGIN

Alignment Scores:
Pred. No.:              1.82e-277      Length:         3208
Score:                  2582.00        Matches:        502
Percent Similarity:     95.3%          Conservative:   21
Best Local Similarity:  91.4%          Mismatches:     26
Query Match:            38.0%          Indels:         0
DB:                     4              Gaps:           0

US-09-976-858-42 (1-1325) x AK032802 (1-3208)

Qy        777 LeuPheGlyIleAlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThr 796
              |||||||||||||||||||||||||||||||||||:::|||||||||:::||||||||||
Db          2 CTTTTTGGCATAGCGAGATCCCTACTGGTGTTCTATATCCTTGTGAACGCTTCCCAGACT 61

Qy        797 LeuHisAsnLysMetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsn 816
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Db         62 TTGCACAACAGGATGTTTGAGTCCATACTGAAGGCTCCCGTGTTGTTCTTCGACAGAAAT 121

Qy        817 ProIleGlyArgIleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeu 836
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Qy        837 ProLeuThrPheLeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerVal 856
              ||||||||||||||||||||||||||||||||||||||||||    |||::::::|||
Db        182 CCCCTGACGTTCCTGGACTTCATCCAGACGTTGCTCCTCGTCGTAAGTGTGATCGCTGTG 241

Qy        857 AlaValAlaValIleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIle 876
              |||   ||||||||||||||||||   ||||||||||||||||||   ::::::|||:::
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Qy        877 PheLeuArgArgTyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThr 896
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Qy        897 ArgSerProValPheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAla 916
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Qy        917 TyrLysAlaGluGluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGlu 936
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Qy        937 AlaTrpPheLeuPheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCys 956
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Qy        957 AlaMetPheValIleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAla 976
              |||:::|||||||||:::||||||||||||||||:::|||||||||||||||:::|||
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Qy        977 GlyGlnValGlyLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCys 996
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Qy       1017 ThrAspLeuGluLysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpPro 1036
              |||||||||||||||||||||||||||||     :::||||||||||||||    ||||||
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Qy       1037 HisGluGlyValIleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeu 1056
              |||||||||||||||:::||||||||||||||||||   ||||||     |||||||||
Db        782 CACGAGGGAGTCATCGTCTTCGACAATGTGAACTTCACCTACAGCTTAGATGGGCCTCTG 841

Qy       1057 ValLeuLysHisLeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArg 1076
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        842 GTTCTGAAGCACCTGACTGCGCTCATCAAGTCCAGGGAAAAGGTTGGAATTGTGGGCAGA 901

Qy       1077 ThrGlyAlaGlyLysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGly 1096
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Qy       1097 LysIleTrpIleAspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLys 1116
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Qy       1157 GluThrIleGluAspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsn 1176
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RESULT 6
AK029876
LOCUS       AK029876                5920 bp    mRNA    linear   HTC 03-APR-2004
```

```
DEFINITION  Mus musculus adult male testis cDNA, RIKEN full-length enriched
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ACCESSION   AK029876
VERSION     AK029876.1  GI:26325799
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 5920)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
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                     APVLLVSPTLLGITMLLATFLIQLERRKGVQSSGIMLTFWLVALLCALAILRSKIISA
                     LKKDAHVDVFRDSTFYLYFTLVLVQLVLSCFSDCSPLFSETVHDRNPCPESSASFLSR
                     ITFWWITGMMVHGYRQPLESSDLWSLNKEDTSEEVVPVLVNNWKKECDKSRKQPVRIV
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ORIGIN

Alignment Scores:
Pred. No.:              3.94e-241     Length:        5920
Score:                  2263.00       Matches:       491
Percent Similarity:     57.3%         Conservative:  288
Best Local Similarity:  36.1%         Mismatches:    468
Query Match:            33.3%         Indels:        112
DB:                     4             Gaps:          23

US-09-976-858-42 (1-1325) x AK029876 (1-5920)

Qy          3 ProValTyrGlnGluVal------------LysProAsnProLeuGlnAspAlaAsnLeu 18
              |||::::::   |||                  |||   |||         |||:::
Db        625 CCCCTGTTCTCTGAAACTGTCCATGACCGGAATCCATGCCCAGAATCCAGTGCCTCTTTC 684

Qy         19 CysSerArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArg 38
                 ||||||:::   |||||||||:::      :::         |||:::::::::
Db        685 CTTTCCAGGATTACTTTCTGGTGGATTACAGGGATGATGGTGCACGGCTACCGCCAGCCC 744

Qy         39 LeuGluGluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGlu 58
              ||||||      |||::::::|||:::      ||||||   |||:::   :::
Db        745 CTGGAGAGCAGTGACCTCTGGTCATTGAATAAGGAGGACACATCAGAAGAAGTGGTACCT 804
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Qy       59 GluLeuGlnGlyPheTrpAspLysGlu-------------------------------- 67
Db      805 GTGCTGGTGAATAACTGGAAGAAGGAATGTGATAAGTCAAGGAAGCAGCCTGTACGGATT 864

Qy       67 ------------------------------------------------------------ 67
Db      865 GTGTATGCCCCTCCCAAAGATCCCAGCAAGCCTAAGGGAAGTTCCCAGTTGGATGTGAAT 924

Qy       68 ------------------ValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThr 81
Db      925 GAGGAGGTGGAGGCACTGATTGTCAAGTCACCCCACAAGGATCGGGAGCCCTCTCTGTTC 984

Qy       82 ArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIle 101
Db      985 AAGGTGTTATACAAGACTTTTGGTCCCTACTTCCTCATGAGCTTCCTGTACAAGGCCCTT 1044

Qy      102 GluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGlu 121
Db     1045 CATGACCTGATGATGTTTGCCGGCCCCAAGATCTTGGAATTGATTATCAACTTCGTGAAT 1104

Qy      122 AsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeu 141
Db     1105 GACAGGGAGGCTCCCGACTGG------------CAGGGCTACTTTTACACAGCACTGCTG 1152

Qy      142 ThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCys 161
Db     1153 TTTGTCAGCGCCTGTCTGCAGACACTGGCACTCCACCAGTACTTTCATATCTGCTTCGTC 1212

Qy      162 AlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeu 181
Db     1213 AGTGGCATGCGCATCAAGACTGCTGTGGTGGGCGCTGTCTATCGTAAGGCTCTTTTGATC 1272

Qy      182 SerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAsp 201
Db     1273 ACCAATGCAGCTAGAAAATCTTCCACGGTCGGAGAGATTGTCAACCTCATGTCCGTGGAT 1332

Qy      202 ValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGln 221
Db     1333 GCTCAGCGCTTCATGGACTTGGCCACGTACATTAACATGATCTGGTCAGCCCCTCTGCAA 1392

Qy      222 AlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMet 241
Db     1393 GTCATCCTAGCCCTCTACTTCCTGTGGCTGAGCCTGGGCCCTTCTGTGCTGGCTGGAGTG 1452

Qy      242 AlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeu 261
Db     1453 GCTGTGATGATTCTCATGGTACCCTTAAATGCTGTG---------------------ATG 1491

Qy      262 ArgSerLysThrAlaThrPhe---------------------ThrAspAlaArgIleArg 274
Db     1492 GCCATGAAGACCAAGACCTACCAGGTGGCACACATGAAGAGCAAAGACAACCGAATCAAG 1551

Qy      275 ThrMetAsnGluValIleThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSer 294
Db     1552 CTGATGAACGAGATCCTCAATGGGATCAAAGTCCTCAAGCTGTACGCCTGGGAGCTGGCC 1611

Qy      295 PheSerAsnLeuIleThrAsnLeuArgLysLysGluIleSerLysIleLeuArgSerSer 314
Db     1612 TTCCAGGACAAAGTCATGAGCATCAGGCAGGAGGAGCTCAAGGTGCTGAAGAAATCTGCC 1671

Qy      315 CysLeuArgGlyMetAsnLeuAlaSerPhePheSerAlaSerLysIleIleValPheVal 334
Db     1672 TACTTGGCAGCTGTAGGCACATTCACGTGGGTGTGCACACCTTTCCTGGTGGCCCTGTCA 1731

Qy      335 ThrPheThrThrTyrValLeuLeuGly------SerValIleThrAlaSerArgValPhe 352
Db     1732 ACCTTTGCTGTCTTTGTGACTGTGGATGAGAGAAATATCCTAGATGCAAAGAAAGCCTTT 1791

Qy      353 ValAlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePheProSerAla 372
Db     1792 GTGTCCCTAGCCCTGTTCAATATCTTGCGCTTCCCACTCAACATC---CTGCCCATGGTT 1848

Qy      373 IleGluArgValSerGluAlaIleValSerIleArgArgIleGlnThrPheLeuLeuLeu 392
Db     1849 ATCAGCAGCATTGTGCAGGCCAGCGTGTCCCTCAAGCGTCTCAGGATTTTCTGTCTCAT 1908

Qy      393 AspGluIle---------SerGlnArgAsnArgGlnLeuProSerAspGlyLysLysMet 409
Db     1909 GAGGAGCTGGAGCCAGACAGCATTGAGCGGAGGTCGATCAAGAGTGGCGAAGGGAATAGC 1968

Qy      410 ValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThrProThrLeuGln 429
Db     1969 ATCACTGTGAAGAATGCAACCTTCACTTGGGCCAGG---GGTGAACCTCCCACACTGAAT 2025

Qy      430 GlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGlyProValGlyAla 449
Db     2026 GGCATCACCTTCTCCATTCCTGAAGGAGCCCTTGTGGCCGTGGTGGGCCAGGTAGGCTGC 2085

Qy      450 GlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHisGlyLeuVal 469
Db     2086 GGGAAGTCATCTCTGCTGTCAGCCCTGCTGGCTGAGATGGACAAGGTGGAGGGACATGTG 2145

Qy      470 SerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPheSerGlyThrLeu 489
Db     2146 ACTCTCAAGGGCTCCGTGGCCTACGTGCCCCAGCAGGCCTGGATTCAGAATGACTCTCTC 2205

Qy      490 ArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGluLysValIleLys 509
Db     2206 CGAGAGAACATACTGTTTGGGCACCCCCTGCAGGAAAATTACTACAAGGCAGTTATGGAA 2265

Qy      510 AlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThrValIleGly 529
Db     2266 GCCTGTGCCCTTCTTCCAGATTTGGAAATCCTGCCCAGTGGGGACCGCACAGAGATCGGT 2325

Qy      530 AspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAlaVal 549
Db     2326 GAGAAGGGTGTGAACCTGTCAGGGGGCCAGAAGCAGCGTGTGAGCCTGGCCCGGGCTGTG 2385

Qy      550 TyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGluVal 569
Db     2386 TACTCTAACTCTGACATCTACCTCTTTGATGACCCCCTCTCGGCTGTGGATGCACATGTT 2445

Qy      570 SerArgHisLeuPheGluLeuCysIle------CysGlnIleLeuHisGluLysIleThr 587
Db     2446 GGGAAGCACATCTTTGAGAAGGTGGTTGGTCCCATGGGCCTACTGAAGAACAAGACACGG 2505

Qy      588 IleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIleLeuLys 607
Db     2506 ATCCTGGTCACCCATGGTATCAGCTACCTGCCCCAAGTGGATGTCATCATTGTCATGAGT 2565

Qy      608 AspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIleAspPhe 627
Db     2566 GGCGGCAAGATCTCAGAGATGGGTTCTTATCAGGAGCTGCTAGACCGGGATGGGGCCTTC 2625

Qy      628 GlySerLeuLeuLys--------------------------------LysAspAsnGlu 636
Db     2626 GCTGAGTTCCTGCGCACCTATGCCAACGCTGAGCAGGACCTGGCCTCGGAGGATGACAGT 2685

Qy      637 GluSer------------GluGlnProProValProGly------------ThrProThr 648
Db     2686 GTCAGTGGTTCAGGGAAGGAGTCAAAGCCGGTGGAAAATGGGATGCTGGTGACAGACACC 2745

Qy      649 Leu---------ArgAsnArgThrPheSerGluSerSerValTrpSerGlnGlnSerSer 665
Db     2746 GTAGGAAAGCACCTGCAGAGGCATCTCAGCAACTCGTCTTCCCACAGTGGGGATACCAGC 2805

Qy      666 ArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnValProValThr 685
Db     2806 CAGCAACACAGCAGCATAGCCGAACTGCAGAAGGCTGGAGCTAAGGAGGAGACGTGGAAG 2865

Qy      686 LeuSerGluGluAsnArgSerGlu---GlyLysValGlyPheGlnAlaTyrLysAsnTyr 704
Db     2866 CTAATGGAAGCAGACAAGGCCCAGACAGGGCAGGTGCAGCTGTCAGTGTACTGGAACTAC 2925

Qy      705 PheArgAlaGlyAlaHisTrpIleValPhe------IlePheLeuIleLeuLeuAsnThr 722
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Db       2926 ATGAAGGCCATTGGCCTCTTCATCACCTTCTTGAGTATCTTCCTTTTCCTGTGCAAC--- 2982

Qy        723 AlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGln 742
                       |||:::   :::     ::::::||||||||  |||    :::
Db       2983 ------CATGTATCTGCACTGGCCTCTAACTATTGGCTGAGCCTCTGGACAGATGACCCC 3036

Qy        743 SerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsn 762
                 ::::::|||  |||                                :::   :::   |||
Db       3037 CCTGTTGTCAATGGGACT--------------------------CAGGCGAACAGGAAT 3069

Qy        763 TrpTyrLeuGlyIleTyrSer------GlyLeuThrValAlaThrValLeuPheGlyIle 780
              :::    |||   :::|||        |||:::              :::||||||
Db       3070 TTTCGGCTGAGTGTCTATGGGGCCTTAGGCATCTTGCAAGGTGCAGCAATATTTGGCTAC 3129

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
              :::   ::::::   :::         :::          :::|||:::   ||||||
Db       3130 TCCATGGCTGTGTCCATCGGGGGCATCTT------GCCTCCCGTCGCTTGCACCTGGAC 3183

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
              :::     ::::::|||::::::|||:::   ||||||:::|||    |||    |||
Db       3184 CTGCTATACAATGTTCTGCGATCACCCATGAGTTTCTTTGAGCGTACACCCAGTGGGAAC 3243

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
              ::::::||||||||||||||||::::::          :::|||    ::::::|||
Db       3244 CTAGTGAACCGATTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCGCAGGTCATC 3303

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
                 |||:::   :::|||        |||:::|||   |||      :::   :::
Db       3304 AAGATGTTCATGGGTTCACTCTTCAGTGTCATTGGAGCTGTCATCATCATCCTACTGGCC 3363

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
                 |||      |||:::   :::   ||||||||:::::::::   |||::::::|||
Db       3364 ACGCCCATTGCCGCAGTCATCATCCCACCCTTGGGTCTGGTTTACTTCTTTGTGCAGAGG 3423

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
              :::::::::   :::||||||   :::||||||||||||||   :::||||||||||||
Db       3424 TTCTATGTGGCTTCCTCAAGACAACTGAAGCGCCTGGAGTCTGTCAGCCGTTCCCCTGTG 3483

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
              :::||||||   :::   :::|||   |||:::      |||||||||::::::   :::
Db       3484 TACTCACACTTCAATGAGACCTTGCTGGGAGTCAGTGTCATCCGTGCTTTTGAGGAGCAG 3543

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
              ||||||                  |||      :::   :::|||::::::
Db       3544 GAGCGCTTCATTCACCAGAGTGACCTGAAAGTAGATGAGAACCAGAAGGCCTACTACCCC 3603

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
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Db       3604 AGCATTGTGGCCAACAGGTGGCTTGCTGTGCGCCTTGAGTGTGTGGGCAACTGCATTGTG 3663

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
              :::      |||      ::::::|||         :::|||   ||||||   ||||||
Db       3664 CTGTTTGCTGCCCTCTTTGCAGTCATCTCCCGGCACAGCCTCAGTGCTGGCTTGGTGGGC 3723

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
              |||::::::||||||:::|||   :::                |||   ||||||   |||
Db       3724 CTCTCTGTGTCTTACTCACTGCAGATAACTGCATACTTGAACTGGCTGGTTCGAATGTCC 3783

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
              :::|||:::|||         :::::::::|||||||||:::      |||      |||
Db       3784 TCGGAGATGGAGACCAACATTGTGGCAGTGGAGAGACTGAAGGAGTATTCTGAAACAGAG 3843

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAla---TrpProHisGluGly 1039
              |||||||||||||||:::      |||:::       ||||||:::   ||||||||   |||
Db       3844 AAGGAGGCTCCTTGGCAAATCCAGGAAACAGCTCCACCCAGCACCTGGCCCCATTCAGGC 3903

Qy       1040 ValIleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLys 1059
                 :::   |||   :::                  |||         ||||||||||||
Db       3904 CGTGTAGAGTTCCGGGATTACTGCCTGAGGTATCGAGAAGACTTGGACTTGGTTCTCAAG 3963

Qy       1060 HisLeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAla 1079
              |||:::         |||:::      |||||||||||||||||||||||||||||||||
Db       3964 CACATAAATGTCACCATTGAGGGTGGAGAAAAGGTGGGTATTGTAGGTCGTACGGGAGCT 4023

Qy       1080 GlyLysSerSerLeuIleSerAlaLeuPheArgLeuSerGlu---ProGluGlyLysIle 1098
              ||||||||||||||||||         ||||||||||::::::|||      ||||||:::|||
Db       4024 GGGAAATCATCTCTCACCCTGGGTTTGTTCCGGATCAATGAGTCTGCAGAAGGGGAGATC 4083

Qy       1099 TrpIleAspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSer 1118
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Db       4084 ATCATTGATGGGGTCAACATCGCCAAGATCGGCCTGCACAACCTGCGCTTCAAGATCACC 4143

Qy       1119 IleIleProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPhe 1138
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Db       4144 ATCATTCCACAGGATCCTGTTTTGTTCTCGGGTTCCCTCCGCATGAACTTGGACCCTTTC 4203

Qy       1139 AsnGluHisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThr 1158
              ::::::::::::|||||||||:::|||   ||||||:::                ||||||
Db       4204 AGTCAGTATTCTGATGAAGAAGTCTGGATGGCCCTGGAGCTTGCTCACCTAAAGGGCTTT 4263

Qy       1159 IleGluAspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSer 1178
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Db       4264 GTGTCAGCTTTGCCTGACAAGCTGAACCATGAGTGTGCAGAAGGTGGAGAGAACCTGAGT 4323

Qy       1179 ValGlyGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeu 1198
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Db       4324 GTGGGGCAGCGACAGCTTGTGTGCCTGGCCCGGGCTCTGCTGAGGAAGACAAAGATTCTA 4383

Qy       1199 IleIleAspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLys 1218
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Db       4384 GTGTTGGACGAGGCTACCGCAGCTGTGGACCTAGAGACAGATAACCTTATCCAGTCCACC 4443

Qy       1219 IleArgGluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIle 1238
              ||||||   :::|||   |||||||||||||||||||||||||||||||||||||||||||
Db       4444 ATCCGGACACAGTTTGAAGACTGTACTGTGCTCACGATTGCTCATCGGCTTAACACCATA 4503

Qy       1239 IleAspSerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluPro 1258
              :::|||      :::::::::|||||||||   |||   ::::::|||         |||
Db       4504 ATGGACTACACGCGGGTGATTGTCCTGGACAAAGGAGAAGTTCGGGAGTGTGGTGCACCC 4563

Qy       1259 TyrValLeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGly 1277
                    ||||||||   :::      :::||||||   |||   :::      |||
Db       4564 TCTGAGCTCCTGCAGCAAAGA---GGCATCTTCTACAGCATGGCCAAGGATGCTGGC 4617
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RESULT 7
CR749835

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LOCUS       CR749835              5899 bp    mRNA    linear   HTC 22-SEP-2004
DEFINITION  Homo sapiens mRNA; cDNA DKFZp781G125 (from clone DKFZp781G125).
ACCESSION   CR749835
VERSION     CR749835.1  GI:51491254
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 5899)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  CONSRTM   The German cDNA Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by BMFZ (Biomedical Research Center at the
            Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA
            sequencing consortium of the German Genome Project. This clone
            (DKFZp781G125) is available at the RZPD Deutsches Ressourcenzentrum
            fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD
            for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp781G125
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
     source          1..5899
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ORIGIN

Alignment Scores:
Pred. No.:              6.61e-236       Length:         5899
Score:                  2216.50         Matches:        519
Percent Similarity:     56.3%           Conservative:   263
Best Local Similarity:  37.4%           Mismatches:     474
Query Match:            32.7%           Indels:         134
DB:                     4               Gaps:           30

US-09-976-858-42 (1-1325) x CR749835 (1-5899)

Qy         38 ArgLeuGluGluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGly 57
              ||||||          |||:::::::|||:::          ||||||    |||:::   :::
Db        156 CGTCTGCTGGGCAGTGACCTCTGGTCCTTAAACAAGGAGGACACGTCGGAACAAGTCGTG 215

Qy         58 GluGluLeuGlnGlyPheTrpAspLysGlu------------------------------ 67
                       |||         |||   ||||||
Db        216 CCTGTTTTGGTAAAGAACTGGAAGAAGGAATGCGCCAAGACTAGGAAGCAGCCAGTGAAG 275

Qy         68 ---ValLeuArgAlaGluAsnAspAlaGln------------------------------ 76
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Db        276 GTCGTGTACTCCTCCAAGGATCCTGCCCAGCCGAAAGAGAGTTCCAAGGTGGATGCGAAT 335

Qy         77 ---------------------------------------------LysProSerLeuThr 81
                                                           |||||||||
Db        336 GAGGAGGTGGAGGCTTTGATCGTCAAGTCCCCACAGAAGGAGTGGAACCCCTCTCTGTTT 395

Qy         82 ArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIle 101
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Qy        102 GluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGlu 121
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Db        456 CACGACCTGATGATGTTTTCCGGGCCGCAGATCTTA---AAGTTGCTCATCAAGTTCGTG 512

Qy        122 AsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeu 141
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Db        513 AAC------------GACACGAAGGCCCCAGACTGGCAGGGCTACTTCTACACCGTGCTG 560

Qy        142 ThrPheCysThrLeuIleLeu---AlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
                |||   |||        |||       ::::::    |||    ||||||:::
Db        561 CTGTTTGTCACTGCCTGCCTGCAGACCCTCGTGCTGCACCAGTACTTCCACATCTGCTTC 620

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
                 :::|||||||||::::::    |||:::       ::|||||||||||||||
Db        621 GTCAGTGGCATGAGGATCAAGACCGCTGTCATTGGGGCTGTCTATCGGAAGGCCCTGGTG 680

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ::::::|||   |||          :::|||     |||:::||||||||||||:::|||
Db        681 ATCACCAATTCAGCCAGAAAATCCTCCACGGTCGGGGAGATTGTCAACCTCATGTCTGTG 740

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              |||       :::|||      :::       :::::::::    :::|||:::   ||||||
Db        741 GACGCTCAGAGGTTCATGGACTTGGCCACGTACATTAACATGATCTGGTCAGCCCCCCTG 800

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              |||    |||          |||||||||:::       :::|||    |||    |||||||||
Db        801 CAAGTCATCCTTGCTCTCTACCTCCTGTGGCTGAATCTGGGCCCTTCCGTCCTGGCTGGA 860

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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Db        861 GTGGCGGTGATGGTCCTCATGGTGCCCGTCAATGCTGTG--------------------- 899

Qy        261 LeuArgSerLysThrAlaThrPhe---------------------ThrAspAlaArgIle 273
              :::          ||||||    |||:::                          |||    ||||||
Db        900 ATGGCGATGAAGACCAAGACGTATCAGGTGGCCCACATGAAGAGCAAAGACAATCGGATC 959

Qy        274 ArgThrMetAsnGluValIleThrGlyIleArgIleIleLysMetTyrAlaTrpGluLys 293
              :::       |||||||||::::::     ||||||:::::::::|||:::||||||||||||
Db        960 AAGCTGATGAACGAAATTCTCAATGGGATCAAAGTGCTAAAGCTTTATGCCTGGGAGCTG 1019

Qy        294 SerPheSerAsnLeuIleThrAsnLeuArgLysLysGluIleSerLysIleLeuArgSer 313
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Db       1020 GCATTCAAGGACAAGGTGCTGGCCATCAGGCAGGAGGAGCTGAAGGTGCTGAAGAAGTCT 1079

Qy        314 SerCysLeuArgGlyMetAsnLeuAlaSerPhePheSerAlaSerLysIleIleValPhe 333
              :::    |||                   ::::::.              ::::::
Db       1080 GCCTACCTGTCAGCCGTGGGCACCTTCACCTGGGTCTGCACGCCCTTTCTGGTGGCCCTG 1139

Qy        334 ValThrPheThrThrTyrValLeuLeu------GlySerValIleThrAlaSerArgVal 351
                 ||||||    ||||||                  :::::::::    |||
Db       1140 TGCACATTTGCCGTCTATGTGACCATTGACGAGAACAACATCCTGGATGCCCAGACAGCC 1199

Qy        352 PheValAlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePheProSer 371
              ||||||::::::    |||:::          :::|||       :::    :::         |||
Db       1200 TTCGTGTCTTTGGCCTTGTTCAACATCCTCCGGTTTCCCCTGAACATT---CTCCCCATG 1256

Qy        372 AlaIleGluArgValSerGluAlaIleValSerIleArgArgIleGlnThrPheLeuLeu 391
                 |||      :::    :::|||    ||||||::::::|||::::::       ||||||
Db       1257 GTCATCAGCAGCATCGTGCAGGCGAGTGTCTCCCTCAAACGCCTGAGGATCTTTCTCTCC 1316

Qy        392 LeuAspGluIleSer------------GlnArgAsnArgGlnLeuProSerAspGlyLys 407
              :::|||:::                     :::|||
Db       1317 CATGAGGAGCTGGAACCTGACAGCATCGAGCGACGGCCTGTCAAAGACGGCGGGGGCACG 1376

Qy        408 LysMetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThrProThr 427
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Db       1377 AACAGCATCACCGTGAGGAATGCCACATTCACCTGGGCCAGG---AGCGACCCTCCCACA 1433

Qy        428 LeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGlyProVal 447
              |||    |||::::::|||::::::          |||    |||:::||||||||||||    |||
Db       1434 CTGAATGGCATCACCTTCTCCATCCCCGAAGGTGCTTTGGTGGCCGTGGTGGGCCAGGTG 1493

Qy        448 GlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHisGly 467
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Db   1494 GGCTGCGGAAAGTCGTCCCTGCTCTCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGG 1553

Qy    468 LeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPheSerGly 487
Db   1554 CACGTGGCTATCAAGGGCTCCGTGGCCTATGTGCCACAGCAGGCCTGGATTCAGAAGGAT 1613

Qy    488 ThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGluLysVal 507
Db   1614 TCTCTCCGAGAAAACATCCTTTTTGGATGTCAGCTGGAGGAACCATATTACAGGTCCGTG 1673

Qy    508 IleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThrVal 527
Db   1674 ATACAGGCCTGTGCCCTCCTCCCAGACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAG 1733

Qy    528 IleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAlaArg 547
Db   1734 ATTGGCGAGAAGGGCGTGAACCTGTCTGGGGGCCAGAAGCAGCGCGTGAGCCTGGCCCGG 1793

Qy    548 AlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAla 567
Db   1794 GCCGTGTACTCCAACGCTGACATTTACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCC 1853

Qy    568 GluValSerArgHisLeuPheGluLeuCysIleCysGln------IleLeuHisGluLys 585
Db   1854 CATGTGGGAAAACACATCTTTGAAAATGTGATTGGCCCCAAGGGGATGCTGAAGAACAAG 1913

Qy    586 IleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIle 605
Db   1914 ACGCGGATCTTGGTCACGCACAGCATGAGCTACTTGCCGCAGGTGGACGTCATCATCGTC 1973

Qy    606 LeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIle 625
Db   1974 ATGAGTGGCGGCAAGATCTCTGAGATGGGCTCCTACCAGGAGCTGCTGGCTCGAGACGGC 2033

Qy    626 AspPheGlySerLeuLeuLys-----------------------LysAspAsnGluGlu 637
Db   2034 GCCTTCGCTGAGTTCCTGCGTACCTATGCCAGCACAGAGCAGGAGCAGGATGCAGAGGAG 2093

Qy    638 Ser--------------------GluGlnProProValProGly-------------- 645
Db   2094 AACGGCAGCACAGTGATGGACGAGGAGGAAGCAGGGGTCACGGGCGTCAGCGGTCCAGGG 2153

Qy    646 ------ThrProThrLeuArgAsn---------------------------------- 651
Db   2154 AAGGAAGCAAAGCAAATGGAGAATGGCATGCTGGTGACGGACAGTGCAGGGAAGCAACTG 2213

Qy    652 ---ArgThrPheSerGluSerSerValTrpSerGlnGlnSerSerArgProSerLeuLys 670
Db   2214 CAGAGACAGCTCAGCAGCTCCTCCTCCTATAGTGGGACATCAGCAGGCAC------CAC 2267

Qy    671 AspGlyAlaLeuGluSerGlnAspThrGlu---------AsnValProValThrLeuSer 687
Db   2268 AACAGCACCGCAGAACCGCAGAAAGCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATG 2327

Qy    688 GluGluAsnArgSerGlu---GlyLysValGlyPheGlnAlaTyrLysAsnTyrPheArg 706
Db   2328 GAGGCTGACAAGGCGCAGACAGGGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAG 2387

Qy    707 AlaGlyAlaHisTrpIleValPhe------IlePheLeuIleLeuLeuAsnThrAlaAla 724
Db   2388 GCCATCGGACTCTTCATCTCCTTCCTCAGCATCTTCCTTTTCATGTGTAAC--------- 2438

Qy    725 GlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMet 744
Db   2439 CATGTGTCCGCGCTGGCTTCCAACTATTGGCTCAGCCTCTGGACTGAT----------- 2486

Qy    745 LeuAsnValThrValAsnGlyGlyGlyAsnValThrGlu---LysLeuAspLeuAsnTrp 763
Db   2487 ---GACCCCATCGTCAACGGGACTCAGGAGCACACGAAAGTCCGGCTGAGCGTCTATGGA 2543

Qy    764 TyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSer 783
Db   2544 GCCCTGGGCATTTCACAAGGGATCGCCGTG-----------TTTGGCTACTCCATGGCC 2591

Qy    784 LeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGlu 803
Db   2592 GTGTCCATCGGGGGGATCTTG------GCTTCCCGCTGTCTGCACGTGGACCTGCTGCAC 2645

Qy    804 SerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsn 823
Db   2646 AGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACCCCCAGTGGGAACCTGGTGAAC 2705

Qy    824 ArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPhe 843
Db   2706 CGCTTCTCCAAGGAGCTGGGCACAGTGGACTCCATGATCCCGGAGGTCATCAAGATGTTC 2765

Qy    844 IleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaValIleProTrp 863
Db   2766 ATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTTATCCTGCTGGCCACGCCCATC 2825

Qy    864 IleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeu 883
Db   2826 GCCGCCATCATCATCCCGCCCCTTGGCCTCATCTACTTCTTCGTCCAGAGGTTCTACGTG 2885

Qy    884 GluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSerHis 903
Db   2886 GCTTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGCCGCTCCCCGGTCTATTCCCAT 2945

Qy    904 LeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArgCys 923
Db   2946 TTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCCTTCGAGGAGCAGGAGCGCTTC 3005

Qy    924 GlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThr 943
Db   3006 ATCCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAGGCCTATTACCCCAGCATCGTG 3065

Qy    944 ThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIleVal 963
Db   3066 GCCAACAGGTGGCTGGCCGTGCGGCTGGAGTGTGTGGGCAACTGCATCGTTCTGTTTGCT 3125

Qy    964 AlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAlaLeu 983
Db   3126 GCCCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCTGGCTTGGTGGGCCTCTCAGTG 3185

Qy    984 SerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGluVal 1003
Db   3186 TCTTACTCATTGCAGGTCACCACGTACTTGAACTGGCTGGTTCGGATGTCATCTGAAATG 3245

Qy   1004 GluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGluAla 1023
Db   3246 GAAACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTATTCAGAGACTGAGAAGGAGGCG 3305

Qy   1024 ProTrpGluTyrGlnLys---ArgProProProAlaTrpProHisGluGlyValIleIle 1042
Db   3306 CCCTGGCAAATCCAGGAGACAGCTCCGCCCAGCAGCTGGCCCCAGGTGGGCCGAGTGGAA 3365

Qy   1043 PheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThr 1062
Db   3366 TTCCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGACTTCGTTCTCAGGCACATCAAT 3425

Qy   1063 AlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSer 1082
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Qy   1083 SerLeuIleSerAlaLeuPheArgLeuSerGlu---ProGluGlyLysIleTrpIleAsp 1101
Db   3486 TCCCTGACCCTGGGCTTATTTCGGATCAACGAGTCTGCCGAAGGAGAGATCATCATCGAT 3545

Qy   1102 LysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIlePro 1121
Db   3546 GGCATCAACATCGCCAAGATCGGCCTGCACGACCTCCGCTTCAAGATCACCATCATCCCC 3605

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Qy       1142 ThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAsp 1161
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Db       3666 TCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCACCTGAAGGACTTCGTGTCAGCC 3725

Qy       1162 LeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGln 1181
              ||||||   |||:::|||   |||   ||||||   |||   |||   ||||||||||||
Db       3726 CTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGGGAGAACCTCAGTGTCGGGCAG 3785

Qy       1182 ArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAsp 1201
              ||||||||||||||||||||||||||||:::|||||||||   :::||||||::::::|||
Db       3786 CGCCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAAGACGAAGATCCTTGTGTTGGAT 3845

Qy       1202 GluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGlu 1221
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Db       3846 GAGGCCACGGCAGCCGTGGACCTGGAAACGGACGACCTCATCCAGTCCACCATCCGGACA 3905

Qy       1222 LysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSer 1241
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Db       3906 CAGTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGGCTCAACACCATCATGGACTAC 3965

Qy       1242 AspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeu 1261
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Db       3966 ACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAGTACGGCGCCCCATCGGACCTC 4025

Qy       1262 LeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGly---------Lys 1278
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Db       4026 CTGCAGCAGAGA---GGTCTTTTCTACAGCATGGCCAAAGACGCCGGCTTGGTGTGAGCC 4082

Qy       1279 AlaGluAlaAlaAlaLeuThrGluThrAlaLysGlnValTyr---------PheLysArg 1295
                 |||   |||   |||      ||||||         :::               :::
Db       4083 CCAGAGCTGGCATATCTGGTCAGAACTGCAGGGCCTATATGCCAGCGCCCAGGGAGGAGT 4142

Qy       1296 AsnTyrProHisIleGlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnPro 1315
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Db       4143 CAGTACCCCTG-GTAAACCAAGCCTCCCACACTGAAACCAAAACATAAAAACCAAACCCA 4201

Qy       1316 SerThrLeuThrIlePheGluThrAla 1324
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Db       4202 GACAACCAAAACATATTCAAAGCAGCA 4228

RESULT 8
BC046560
LOCUS       BC046560                4547 bp    mRNA    linear   HTC 19-NOV-2003
DEFINITION  Mus musculus ATP-binding cassette, sub-family C (CFTR/MRP), member
            3, mRNA (cDNA clone IMAGE:4194166), containing frame-shift errors.
ACCESSION   BC046560
VERSION     BC046560.1  GI:28279835
KEYWORDS    HTC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4547)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 4547)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-FEB-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 92 Row: f Column: 22
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4194166"
                     /tissue_type="Liver, normal. 5 month old male mouse."
                     /clone_lib="NCI_CGAP_Li9"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN

Alignment Scores:
Pred. No.:              5.86e-228     Length:         4547
Score:                  2144.00       Matches:        483
Percent Similarity:     56.4%         Conservative:   283
Best Local Similarity:  35.6%         Mismatches:     479
Query Match:            31.6%         Indels:         114
DB:                     4             Gaps:           24

US-09-976-858-42 (1-1325) x BC046560 (1-4547)

Qy          3 ProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSerArgVal 22
              |||         :::         |||   |||         |||         ||||||:::
Db        160 CCGGAGAATCTTGACACAAATCCTTGCCCAGAGGCCAGCGCTGGCTTCTTTTCCCGCTTG 219

Qy         23 PhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGluGluAsp 42
               |||||||||         |||         :::|||::::::|||   ||||||:::
Db        220 TCTTTCTGGTGGTTCACAAGGCTTGCCATCCTTGGCTACCGACGTCCCCTGGAGGACCGT 279

Qy         43 AspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeuGlnGly 62
              |||::::::|||:::      ||||||   |||         :::   :::   |||
Db        280 GACCTCTGGTCTCTGTCTGAGGAGGACTGCTCTCACAAGGTGGTACAACGGCTGCTGGAA 339

Qy         63 PheTrpAspLysGlu--------------------------------------------- 67
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Db        340 GCATGGCAAAAGCAGCAGAACCAAGCATCAGGGTCCCAGACGGCAACAGCTGAGCCAAAG 399

Qy         68 ---------------------ValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Db        400 ATCCCAGGTGAGGATGCGGTCCTACTGAAGCCCCGACCCAAGTCCAAGCAGCCTTCCTTT 459

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
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Db        460 CTGAGGGCTTTGGTGAGAACCTTCACCTCCAGCTTGCTCATGAGTGCCTGCTTCAACCTG 519

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              |||:::              :::   |||        |||        :::|||   :::
Db        520 ATCCAGAACCTACTCGGCTTCGTCAACCCACAGCTGCTCAGTATACTCATCAGGTTTATT 579

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAla---------------Tyr 135
                       ||||||                      ||||||              :::
Db        580 TCT------GACCCC--------------------ACGGCCCCCACCTGGTGGGGCTTC 612

Qy        136 AlaTyrAlaThrValLeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyr 155
                       |||   ::::::         :::   :::      ::::::   |||   |||
Db        613 TTGCTGGCCGGACTGATGTTCCTGAGCTCCACCATGCAGACATTGATCTTACACCAATAT 672

Qy        156 PheTyrHisValGlnCysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyr 175
              ::::::   :::            :::|||||||||   |||:::      :::||||||
Db        673 TACCACTGCATCTTTGTGATGGCCTTGAGGCTACGGACTGCTATTATAGGTGTCATCTAC 732

Qy        176 ArgLysAlaLeuArgLeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleVal 195
              ||||||||||||     ::::::|||               ::::::|||   |||::::::|||
Db        733 AGGAAGGCTCTGGTCATCACCAACTCAGTCAAACGGGAGTCCACTGTGGGAGAAATGGTC 792

Qy        196 AsnLeuLeuSerAsnAspValAsnLysPheAspGlnValThrValPheLeuHisPheLeu 215
              ||||||:::|||   |||      :::|||   |||:::   |||::::::      |||
Db        793 AACCTCATGTCAGTGGATGCTCAGCGCTTCATGGATGTCTCCCCTTTCATCAATCTGCTG 852

Qy        216 TrpAlaGlyProLeuGlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIle 235
              |||:::   |||||||||   |||                  ||||||      :::|||
Db        853 TGGTCTGCACCTTTGCAGGTCATCCTGGCAATATACTTCCTCTGGCAGATCCTGGGCCCA 912

Qy        236 SerCysLeuAlaGlyMetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGly 255
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Db        913 TCAGCTCTGGCTGGAGTGGCTGTGATAGTCTTGCTGATACCACTCAATGGAGCTGTGTCC 972

Qy        256 LysLeuPheSerSerLeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThr 275
                          :::   :::   |||         |||   |||:::||||||:::
Db        973 ATGAAGATGAAGACCTACCAGGTAAAGCAAATGAAGTTCAAGGACTCCCGCATCAAGCTG 1032

Qy        276 MetAsnGluValIleThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPhe 295
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Db       1033 ATGAGCGAGATCCTGAACGGCATCAAAGTGCTCAAGCTGTACGCTTGGGAGCCCAGCTTC 1092

Qy        296 SerAsnLeuIleThrAsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCys 315
                       :::      :::|||:::   |||:::      :::   :::   :::
Db       1093 TTGGAGCAGGTGAAAGGGATCAGGCAGAGTGAACTTCAGCTGCTCCGGAAGGGGGCCTAC 1152

Qy        316 LeuArgGlyMetAsnLeuAlaSerPhePheSerAlaSerLysIleIleValPheValThr 335
              |||:::   ::::::            :::            ::::::      :::|||
Db       1153 CTGCAGGCCATCTCCACCTTCATCTGGATCTGCACCCCATTTCTGGTGACCCTGATCACC 1212

Qy        336 PheThrThrTyrValLeuLeu------GlySerValIleThrAlaSerArgValPheVal 353
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Db       1213 CTCGGAGTGTACGTGTATGTGGACGAGAGCAATGTACTGGATGCCGAGAAGGCCTTTGTG 1272

Qy        354 AlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePheProSerAlaIle 373
              :::::::::|||:::   :::::::::      :::   :::   |||      |||
Db       1273 TCCCTGTCTTTGTTCAATATCTTAAAGATCCCCCTCAACATG---CTGCCTCAGTTAATC 1329

Qy        374 GluArgValSerGluAlaIleValSerIleArgArgIleGlnThrPheLeuLeuLeuAsp 393
                       :::::::::|||   ||||||:::::::::|||||||||   ||||||      :::
Db       1330 AGTGGACTGACCCAGGCCAGCGTGTCTCTGAAACGGATCCAGGATTTCCTGAACCAAAAT 1389

Qy        394 GluIleSerGlnArg------AsnArgGlnLeuProSerAspGlyLysLysMet---Val 410
              |||:::      :::         |||:::      |||   |||      :::   :::
Db       1390 GAACTTGACCCCCAATGTGTGGAAAGAAAGACCATCTCCCCAGGCTACGCCATCACCATA 1449

Qy        411 HisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThrProThrLeuGlnGly 430
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Db       1450 CACAACGGCACCTTCACC------TGGGCCCAG---GACCTGCCGCCCACCCTGCACAGC 1500

Qy        431 LeuSerPheThrValArgProGlyGluLeuLeuAlaValValGlyProValGlyAlaGly 450
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Db       1501 CTAAACATTCAAATCCCGAAGGGGGCGTTGGTGGCTGTGGTGGGACCTGTGGGCTGTGGG 1560

Qy        451 LysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHisGlyLeuValSer 470
              ||||||||||||:::|||||:::|||||||||:::               |||:::||||||
Db       1561 AAGTCTTCTCTGGTGTCTGCCTTACTCGGAGAGATGGAGAAGCTGGAAGGTGTGGTGTCT 1620

Qy        471 ValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPheSerGlyThrLeuArg 490
              |||   |||   :::|||||||||   ||||||   |||:::   :::   ||||||:::
Db       1621 GTAAAGGGCTCTGTGGCCTACGTGCCCCAGCAGGCATGGATCCAGAACTGCACACTTCAG 1680

Qy        491 SerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGluLysValIleLysAla 510
              |||:::||||||||||:::            :::||||||::::::      ::::::
Db       1681 GAAAATGTGCTATTTGGCCAACCCATGAACCCCAAGCGCTACCAACAGGCTCTGGAGACA 1740

Qy        511 CysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThrValIleGlyAsp 530
              ||||||||      ||||||   :::|||      ||||||   |||   ||||||:::
Db       1741 TGTGCCCTGCTAGCTGACCTAGATGTGCTTCCTGGTGGGGACCAGACAGAGATTGGAGAG 1800

Qy        531 ArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAlaValTyr 550
              :::|||      ||||||||||||||:::   ||||||:::||||||||||||||||||
Db       1801 AAGGGTATTAACCTATCTGGAGGCCAGCGCCAACGGGTGAGTTTGGCCCGAGCTGTTTAT 1860

Qy        551 GlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGluValSer 570
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Db       1861 AGTGATGCCAACATTTTTTTGCTGGATGACCCACTGTCGGCTGTGGACTCTCATGTGGCG 1920

Qy        571 ArgHisLeuPheGluLeuCysIleCysGln------IleLeuHisGluLysIleThrIle 588
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Db       1921 AAGCATATCTTCGACCAAGTGATTGGACCAGAAGGTGTGCTGGCAGGCAAGACTCGGGTG 1980

Qy        589 LeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIleLeuLysAsp 608
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Db       1981 CTGGTAACTCATGGCATCAGCTTCCTGCCCCAGACGGACTTTATCATTGTGCTTGCTGGT 2040

Qy        609 GlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIleAspPheGly 628
              |||::::::   :::   |||   |||:::      |||:::               |||
Db       2041 GGACAGGTGTCTGAGATGGGCCACTACTCGGCCCTCCTGCAGCATGATGGCTCCTTTGCC 2100

Qy        629 SerLeuLeuLys---------------LysAspAsnGluGluSerGlu-GlnPro----- 641
              :::   |||:::               :::|||   |||:::   |||   ||||||
Db       2101 AACTTCCTCCGAAACTACGCACCAGATGAAGACCAGGAGGACCATGAAGCAGCCTTGCAA 2160

Qy        642 ---------------------------ProValProGlyThrProThrLeuArgAsnAr 652
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Db       2161 AATGCAAATGAGGAGGTACTCCTGCTCGAAGACACACTCAGCACCCACACAGACCTGACA 2220

Qy        652 gThrPheSerGluSerSerValTrpSerGlnGlnSerSer------------ArgProSe 668
              :|||   |||:::   |||      |||      ||||||               |||
Db       2221 GACAATGAGCCAGCCATCTACGAGGTCCGCAAGCAGTTCATGAGAGAGATGAGCTCCTTG 2280

Qy        668 rLeuLysAspGlyAlaLeuGluSerGln------------------------------ 677
               |||   :::|||   ::::::::::::
Db       2281 TCTTCT-GAAGGGGAGGTCCAGAACCGGACTATGCCCAAGAAACACACAAATTCATTGGA 2339

Qy        678 ------------------AspThrGluAsnValProValThrLeuSerGluGluAsnAr 691
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Db       2340 GAAGGAGGCGCTGGTGACAAAGACTAAGGAGACTGGCGCATTAATCAAAGAGGAGATAGC 2399

Qy        691 gSerGluGlyLysValGlyPheGlnAlaTyrLysAsnTyrPheArgAlaGlyAlaHisTr 711
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Db       2400 AGAGACAGGCAATGTGAAGCTGAGTGTGTACTGGGATTATGCCAAGTCT---ATGGGACT 2456

Qy        711 pIleValPheIlePheLeuIleLeuLeuAsnThrAlaAlaGlnValAlaTyrValLeuGl 731
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Db       2457 CTGTACCACGCTATCTATCTGCCTCCTGTATGGTGGCCAAAGCGCAGCTGCTATCGGAGC 2516

Qy        731 nAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMetLeuAsnValThrValAsnGl 751
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Db       2517 CAATGTGTGGCTCAGCGCCTGGAGCAAT---------------GATGCGGAGGAACATGG 2561

Qy        751 yGlyGlyAsnValThrGluLysLeuAspLeuAsnTrpTyrLeuGlyIleTyrSerGlyLe 771
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```

```
Qy        771 uThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeuVal------------Ph 787
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Db       2607 A---------------------GGGATACTGCAAGGGCTCCTGGTCATGCTGTCAGCTTT 2645

Qy        787 eTyrValLeuValAsnSerSerGlnThr---------LeuHisAsnLysMetPheGluSe 804
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Db       2646 CACCATGGTGGTCGGCGCGATCCAGGCTGCCCGCCTGCTGCACGAAGCTCTGCTGCACAA 2705

Qy        804 rIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnAr 824
              :   :::::::::|||      ||||||||      |||  |||||||||||||||
Db       2706 CAAGATTCGTTCCCCTCAGTCCTTCTTTGACACCACGCCCTCGGGCCGCATCCTCAACCG 2765

Qy        824 gPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIl 844
              ||||||||||||||||        :::|||::::::|||     |||   |||      ::
Db       2766 TTTCTCCAAGGACATATACGTCATCGACGAGGTTCTGGCCCCCACCATCCTCATGCTGTT 2825

Qy        844 eGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaValIleProTrpIl 864
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Db       2826 GAATTCCTTCTTCACATCCATCTCCACCATCATGGTCATCGTGGCCAGCACGCCGCTCTT 2885

Qy        864 eAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGl 884
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Db       2886 CATGGTGGTTGTCTTGCCCCTGGCTGTGCTCTATGGCTTTGTGCAGCGCTTCTATGTGGC 2945

Qy        884 uThrSerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSerHisLe 904
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Db       2946 CACATCACGGCAGCTCAAGCGGCTGGAATCCATCAGCCGCTCACCCATCTTCTCCCACTT 3005

Qy        904 uSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArgCysGl 924
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Qy        924 nGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrTh 944
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Qy        944 rSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAl 964
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Db       3126 CAATCGATGGCTGGGGGTCCACGTGGAGTTTGTGGGGAACTGCGTGGTGCTCTTTGCCGC 3185

Qy        964 aPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSe 984
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Db       3186 ACTGTTTGCAGTGATCGGGAGAAACAGCTTGAATCCAGGGCTTGTGGGTCTTTCTGTGTC 3245

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Db       3246 CTATGCCTTACAGGTGACCATGGCTTTGAATTGGATGATACGAATGATATCCGACTTGGA 3305

Qy       1004 uAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGluAlaPr 1024
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Db       3306 GTCTAATATCATAGCTGTGGAGAGAGTCAAGGAGTACTCTAAGACCAAGACTGAGGCCCC 3365

Qy       1024 oTrpGluTyrGln---LysArgProProProAlaTrpProHisGluGlyValIleIlePh 1043
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Db       3366 CTGGGTGGTGGAGAGCAACCGCGCCCCGGAAGGCTGGCCCACGCGAGGAATGGTGGAGTT 3425

Qy       1043 eAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAl 1063
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Db       3426 CCGGAACTATTCAGTGCGGTACCGGCCTGGCCTCGAGTTGGTGCTGAAGAACGTGACTGT 3485

Qy       1063 aLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSe 1083
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Db       3486 TCATGTGCAGGGTGGGGAGAAGGTAGGCATTGTGGGCCGCACTGGGGCTGGCAAATCTTC 3545

Qy       1083 rLeuIleSerAlaLeuPheArgLeuSerGlu---ProGluGlyLysIleTrpIleAspLy 1102
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Db       3546 CATGACTCTTTGCCTGTTCCGAATCCTGGAGGCCGCAGAGGGTGAGATCGTCATTGATGG 3605

Qy       1102 sIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGl 1122
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Db       3606 GCTCAACGTGGCACACATTGGCCTCCACGACCTGCGCTCTCAGCTCACCATCATCCCTCA 3665

Qy       1122 nGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisTh 1142
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Db       3666 GGACCCCATCCTGTTCTCGGGCACCCTGCGTATGAACTTAGATCCCTTTGGCCGATACTC 3725

Qy       1142 rAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLe 1162
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Qy       1162 uProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGlnAr 1182
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Db       3786 GCCAGCAGGCCTGGATTTCCAGTGCGCTGAGGGTGGGGATAATCTCAGTGTTGGCCAGAG 3845

Qy       1182 gGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGl 1202
              |||||||||||||||||||||||:::|||||||||:::::::::|||::::::||||
Db       3846 GCAGCTTGTATGCCTAGCCCGAGCCCTGCTCCGGAAGAGCCGAGTCCTGGTTTTAGACGA 3905

Qy       1202 uAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLy 1222
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Qy       1222 sPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAs 1242
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Qy       1242 pLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLe 1262
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Db       4026 CAGGGTCCTGGTCTTGGACAAAGGAGTAGTAGCTGAATTTGATTCTCCAGTCAACCTCAT 4085

Qy       1262 uGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAla 1279
                 :              :::||||||   |||   :::         |||   |||
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RESULT 9
CL969772
LOCUS       CL969772               4953 bp    DNA     linear   GSS 21-SEP-2004
DEFINITION  OsIFCC018842 Oryza sativa Express Library Oryza sativa (indica
            cultivar-group) genomic, genomic survey sequence.
ACCESSION   CL969772
VERSION     CL969772.1  GI:52394164
KEYWORDS    GSS.
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 4953)
  AUTHORS   Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
            Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
            Wong,G.K.S., Deng,X.W. and Wang,J.
  TITLE     An analysis of transcriptional regulation of the rice genome and
            its comparison to Arabidopsis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Chen Chen
            Department of Bioinformatic
            Beijing Institute of Genomics
            Chinese Academy of Sciences, Beijing 101300, China
            Tel: 86-10-80481559
            Fax: 86-10-80488676
            Email: chenchen@genomics.org.cn
            Rice genomic sequence.
            Class: exon-trapped.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:39946"
                     /clone_lib="Oryza sativa Express Library"
                     /note="Oryza sativa exon trapped genomic sequences "
ORIGIN

Alignment Scores:
Pred. No.:              3.23e-227      Length:         4953
Score:                  2138.00        Matches:        481
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Percent Similarity:        56.1%         Conservative:   266
Best Local Similarity:     36.1%         Mismatches:     496
Query Match:               31.5%         Indels:         88
DB:                        10            Gaps:           22

US-09-976-858-42 (1-1325) x CL969772 (1-4953)

Qy          2 LeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSerArg 21
Db        661 CTGCCTGGTGGGGAGCAGATTTGCCCTGAG------AGGCATGCTAATATATTTCCAGG 714

Qy         22 ValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGluGlu 41
Db        715 ATATTCTTTTCATGGATGACTCCTCTAATGCAACAAGGATTTAAAAGGCCCATCACCGAT 774

Qy         42 AspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeuGln 61
Db        775 AAGGATATTTGGAAATTAGACAGTTGGGATGAGACTGAAACATTGTACAACCAGTTCCAA 834

Qy         62 GlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThr 81
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Qy         82 ArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIle 101
Db        880 CGGGCTCTGCATAGCAGCCTTGGTGGAAGGTTTGGCTAGGAGGATTTTTTAAGATTGGC 939

Qy        102 GluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGlu 121
Db        940 AATGATGCTTCTCAGTTGTTGGCCCACTCATATTGAACCTCTTGTTGGAGTCTATGCAA 999

Qy        122 AsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeu 141
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Qy        142 ThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeu---TyrPheTyrHisValGln 160
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Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
Db       1162 CTAACTAATGATAGTCGAAAGAAGTTTGCCTCTGGGAGGATAACCAATTTGATTTCAACT 1221

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Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
Db       1342 GCAGCCATGTTGGTTCTTTTGTTCCCAATTCAGACTGTTATCATAAGCAAAATGCAAAAA 1401

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Db       1402 CTTACCAAGGAAGGGTTGCAAAGGACTGACAGGAGAATCAGTCTAATGAATGAAATATTA 1461

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
Db       1462 GCTGCAATGGATACGGTCAAATGTTATGCTTGGGAGCAAAGTTTCCAGTCAAAAGTGCAG 1521

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
Db       1522 GACATCCGTGATGATGAAATTTCATGGTTCCGCAGCGCTCAATTGCTTGCTGCGCTGAAT 1581

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGlu---------------Ile 395
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Qy        396 SerGlnArgAsnArgGlnLeuProSerAspGlyLysLysMetValHisValGlnAspPhe 415
Db       1819 CCACCTCTTGATCCTGAGCTTCCAGCA---------------ATTTCTATTAAGAATGGA 1863

Qy        416 ThrAlaPheTrpAspLysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrVal 435
Db       1864 TATTTTTCATGGGAATCGCAGGCTGAGAGACCAACATTATCAAACGTCAATCTGGATGTA 1923

Qy        436 ArgProGlyGluLeuLeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeu 455
Db       1924 CCTATGGGCAGTTTGGTTGCAATAGTAGGAAGCACTGGGGAGGGGAAGACTTCTCTTATT 1983

Qy        456 SerAlaValLeuGlyGluLeuAlaPro---------SerHisGlyLeuValSerValHis 472
Db       1984 TCTGCAATGCTTGGTGAAATACCACCAGTGTCAGGATCGAATACATCGGTGGTCCTTCGT 2043

Qy        473 GlyArgIleAlaTyrValSerGlnGlnProTrpValPheSerGlyThrLeuArgSerAsn 492
Db       2044 GGAACAGTGGCTTATGTTCCTCAAGTTTCATGGATCTTCAATGCAACTGTCCGGGACAAT 2103

Qy        493 IleLeuPheGlyLysLysTyrGluLysGluArgTyrGluLysValIleLysAlaCysAla 512
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Qy        513 LeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThrValIleGlyAspArgGly 532
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Qy        533 ThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAlaValTyrGlnAsp 552
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Qy        553 AlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGluValSerArgHis 572
Db       2284 TCAGATGTCTACATATTTGATGATCCACTGAGTGCATTAGATGCCCATGTTGGTCGACAG 2343

Qy        573 Leu----------------------------------------------------------- 573
Db       2344 ATAGGCACACTTTCTGGTTGTTATAGAGTAATTGCGTCGATAAGATATGGTACACCATTT 2403

Qy        574 ---------PheGluLeuCysIleCysGlnIleLeuHisGluLysIleThrIleLeuVal 590
Db       2404 GTCACGGTATTTGACAAATGTATTAAAGAAGAGCTACAGCACAAAACTAGGGTTCTTGTT 2463

Qy        591 ThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIleLeuLysAspGlyLys 610
Db       2464 ACCAATCAGCTGCATTTTCTACCATATGTGGATAAAATACTGGTAGTCCATGATGGTGTA 2523

Qy        611 MetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIleAspPheGlySerLeu 630
Db       2524 ATTAAAGAAGAAGGTACCTTTGATGAACTTAGCAACTCTGGGGAACTCTTTAAGAAGCTC 2583

Qy        631 LeuLysLysAspAsnGluGluSerGluGlnProProValProGlyThrProThrLeuArg 650
Db       2584 ATGGAAAATGCTGGAAAGATGGAAGAACAG---------------ATGGAAGAGAAACAG 2628

Qy        651 AsnArgThrPheSerGluSerSerValTrpSerGlnGlnSerSerArgProSerLeuLys 670
Db       2629 GACGAAAGCAAAAGACAGGATGACATAAAACACCCTGAAAATGGGGGCAGTGTAATAGCT 2688
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Qy        671 AspGlyAlaLeuGlu---SerGlnAspThrGluAsn--------------ValProVal 684
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Db       2689 GATGGTGATATGCAGAAGAGTCAGGACACTTCTAATAAAACAAAACAGGGGAAATCTGTT 2748

Qy        685 ThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLysAsnTyr 704
                 :::  :::|||  |||      |||  :::       :::              |||
Db       2749 CTGATTAAACAAGAAGAAAGGGAAACTGGAGTTATAAGTGCAAAGGTCCTTTCACGCTAC 2808

Qy        705 PheArgAla---GlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAla 723
                       |||   |||    |||:::|||  :::   |||
Db       2809 AAAAATGCATTGGGAGGGATCTGGGTGGTATCTGTT---CTCTTTTTTGCTATGCACTC 2865

Qy        724 AlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSer 743
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Db       2866 ACTGAAGTTCTTCGCATTTCAAGTAGCACATGGTTGAGCGTTTGGACAGATCAAGGTTCT 2925

Qy        744 MetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsnTrp 763
                                 ::::::||| |||                         :::
Db       2926 ---------ACGAAAATCCATGGCCCTGGT--------------------------TAC 2949

Qy        764 TyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSer 783
              |||      ||||||    |||:::            ||||||    :::      |||
Db       2950 TACAATTTAATCTACGGCCTTCTTTCTTTTGGGCAGGTTCTAGTCACTCTAACGAATTCT 3009

Qy        784 LeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGlu 803
                    :::           :::  :::::::::  ||||||:::   |||
Db       3010 TATTGGCTGATCACATCAAGTCTTCGAGCAGCCAAGAGGTTGCATGATGCCATGCTCCGG 3069

Qy        804 SerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsn 823
              |||||||||:::||||||:::::::||||||      ||||||:::|||||||||:::|||
Db       3070 TCTATATTAAGAGCTCCCATGGTATTTTTTCACACCAATCCACTTGGACGAATCATCAAC 3129

Qy        824 ArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeu---------ThrPhe 840
              |||||||||||||||:::|||    :::|||     :::   :::          |||
Db       3130 AGATTTTCAAAGGATTTGGGTGACATTGACAGGAATGTAGCCATCTTTGTGAATATGTTT 3189

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
              :::        |||      ||||||         ::::::   :::          :::
Db       3190 ATGGCACAAATATCTCAGTTGCTCTCAACATTTGTTCTCATTGGCATTGTTAGCACTATG 3249

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
                    |||      :::||||||:::             |||:::|||
Db       3250 TCTCTGTGGGCTATCATGCCACTTCTG---------ATTTTATTTTATGCAGCTTACCTC 3300

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
              |||:::      |||||||||:::||||||||||||:::|||   |||||||||||||||
Db       3301 TATTACCAGACTACGTCTCGTGAGGTAAAGCGCCTGGATTCCATTACAAGGTCTCCTGTG 3360

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Db       3361 TATGCTCAATTTTCAGAGGCATTGAATGGTCTGTCTACAATCCGTGCCTACAAAGCCTAT 3420

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
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Db       3421 GATAGAATGGCAAACATCAATGGGAAATCAATGGACAACAACATCAGATTCACTCTTGTG 3480

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
                 ::::::::::::||||||   |||:::||||||:::   :::      :::   :::
Db       3481 AACATGAGTTCAAACAGATGGCTAGCCATCCGTCTGGAAACATTGGGTGGCATCATGATA 3540

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAsp--------------- 975
                       |||      :::::::::      :::   :::
Db       3541 TGGTTCACAGCAACATTTGCTGTCATGCAAAACCAACGAGCAGAAAATCAAAAGGCTTTT 3600

Qy        976 AlaGlyGlnValGlyLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrp 995
              |||      :::||||||   |||:::|||   |||   :::         :::
Db       3601 GCCTCCACAATGGGTCTTCTTCTTACTTACACCCTCAATATCACCAATTTGCTCACGGCT 3660

Qy        996 CysValArgGlnSerAlaGluValGluAsnMetMetIleSerValGluArgValIleGlu 1015
                 :::|||   ::::::         ||||||   :::   :::||||||||||||
Db       3661 GTTCTTCGTCTTGCTAGTCTGGCTGAAAACAGTTTAAATGCTGTTGAGCGGGTAGGAACA 3720

Qy       1016 TyrThrAspLeuGluLysGluAlaProTrpGluTyrGln---LysArgProProProAla 1034
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Db       3721 TACATTGAGTTGCCTTCTGAGGCTCCTCCTGTCATTGAGGATAGCAGGCCACCTCCTGGT 3780

Qy       1035 TrpProHisGluGlyValIleIlePheAspAsnValAsnPheMetTyrSerProGlyGly 1054
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Db       3781 TGGCCATCATCTGGTGTTGTCAAGTTTGAAGACGTCGTGCTTCGGTACCGACCAGAACTT 3840

Qy       1055 ProLeuValLeuLysHisLeuThrAlaLeuIleLysSerGlnGluLysValGlyIleVal 1074
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Db       3841 CCTCCTGTTCTTCATGGCATATCTTTCATCATTAATGGCAGCGAAAAGGTAGGAATAGTT 3900

Qy       1075 GlyArgThrGlyAlaGlyLysSerSerLeuIleSerAlaLeuPheArgLeuSerGluPro 1094
              |||||||||||||||||||||||||||:::::::::||||||||||||:::    |||
Db       3901 GGCAGAACAGGAGCTGGTAAATCTAGCATGCTGAATGCTCTGTTCCGTATTGTGGAACTG 3960

Qy       1095 Glu---GlyLysIleTrpIleAspLysIleLeuThrThrGluIleGlyLeuHisAspLeu 1113
              |||   |||:::|||   :::|||         |||::::::   |||:::   ||||||
Db       3961 GAACGAGGGAGAATATTGGTTGATGATTGTGACACTTCTAAATTTGGAATTTGGGACCTA 4020

Qy       1114 ArgLysLysMetSerIleIleProGlnGluProValLeuPheThrGlyThrMetArgLys 1133
              ||||||   :::   ||||||||||||   ||||||||||:::|||::::::|||
Db       4021 CGAAAAGTACTAGGAATAATACCACAGGCACCTGTCCTATTTCAGGTTCTGTTCGATTT 4080

Qy       1134 AsnLeuAspProPheAsnGluHisThrAspGluGluLeuTrpAsnAlaLeuGlnGluVal 1153
              ||||||||||||||||||||||||   |||      :::||||||   ||||||:::
Db       4081 AATCTGGATCCTTTTAATGAGCACAATGATGCGGATCTCTGGGAAGCGCTTGAAAGGGCT 4140

Qy       1154 GlnLeuLysGluThrIleGluAspLeuProGlyLysMetAspThrGluLeuAlaGluSer 1173
                    ||||||:::   |||                :::|||   |||::::::|||:::
Db       4141 CATCTAAAAGATGTCATAAGGAGGAATGCTCTGGGACTAGATGCTGAGGTCTCTGAGGCT 4200

Qy       1174 GlySerAsnPheSerValGlyGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArg 1193
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Db       4201 GGTGAAAATTTTAGCGTTGGACAGCGGCAGCTACTGAGTTTAGCTCGTGCATTGCTGCGG 4260

Qy       1194 LysAsnGlnIleLeuIleIleAspGluAlaThrAlaAsnValAspProArgThrAspGlu 1213
              :::   :::||||||:::::::||||||||||||||||   ||||||   |||||||||
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Qy       1214 LeuIleGlnLysLysIleArgGluLysPheAlaHisCysThrValLeuThrIleAlaHis 1233
              ||||||||||||   ||||||||||||:::|||   |||||||||:::|||   |||||||||
Db       4321 CTTATACAGAAGACAATCAGGGAAGAATTCAAGAGTTGTACAATGCTTATAATTGCTCAC 4380

Qy       1234 ArgLeuAsnThrIleIleAspSerAspLysIleMetValLeuAspSerGlyArgLeuLys 1253
              ||||||||||||:::||||||   |||::::::::::::|||   :::|||::::::
Db       4381 CGCCTGAACACTGTTATTGACTGTGACAGGTTGCTTATTCTAAGTGCTGGGAAGGTTTTG 4440

Qy       1254 GluTyrAspGluProTyrValLeuLeuGlnAsnLysGluSerLeuPheTyrLysMetVal 1273
              |||:::|||   |||      ||||||   |||:::   |||   |||   |||||||||
Db       4441 GAGTTCGACTCTCCTGAGAATCTTTTGAGCAATGAGCACAGTGCTTTCTCCAAGATGGTT 4500

Qy       1274 GlnGlnLeuGlyLysAlaGluAlaAlaAlaLeu 1284
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Db       4501 CAGAGTACAGGACCTAGCAATGCAGAGTACCTG 4533
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RESULT 10
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LOCUS       DQ044660                4638 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Homo sapiens ABCC2 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ044660
VERSION     DQ044660.1  GI:66895875
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 4638)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 4638)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
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                     /gene="ABCC2"
                     /locus_tag="HC10881"
ORIGIN

Alignment Scores:
Pred. No.:              5.54e-217      Length:        4638
Score:                  2046.50        Matches:       466
Percent Similarity:     53.9%          Conservative:  258
Best Local Similarity:  34.7%          Mismatches:    499
Query Match:            30.2%          Indels:        119
DB:                     11             Gaps:          19

US-09-976-858-42 (1-1325) x DQ044660 (1-4638)

Qy         34 GlyHisLysArgArgLeuGluGluAspAspMetTyrSerValLeuProGluAspArgSer 53
              |||:::|||||  |||       :::|||::::::  |||      |||   ::::::
Db        646 GGCTACAAGCGTCCTCTGACACTCGAGGATGTCTGGGAAGTTGATGAAGAGATGAAAACC 705

Qy         54 GlnHisLeuGlyGluGluLeuGlnGlyPheTrpAspLysGluValLeuArgAla------ 71
              :::  |||      :::   :::           :::|||:::  :::|||
Db        706 AAGACATTAGTGAGCAAGTTTGAAACGCACATGAAGAGAGAGCTGCAGAAAGCCAGGCGG 765

Qy         71 ------------------------------------------------------------ 71

Db        766 GCACTCCAGAGACGGCAGGAGAAGAGCTCCCAGCAGAACTCTGGAGCCAGGCTGCCTGGC 825

Qy         71 ------------------------------------------------------------ 71

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Qy         72 ------------------GluAsnAspAlaGlnLysProSerLeuThrArgAlaIleIle 85
                                :::   |||      |||      |||   :::|||:::
Db        886 AAAAAGAAGTCTGGGACCAAAAAAGATGTTCCAAAATCCTGGTTGATGAAGGCTCTGTTC 945

Qy         86 LysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGluGluSerAla 105
              |||   ::::::      |||      :::      |||:::   :::
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Qy        106 LysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspPro 125
                 :::   |||      |||      :::|||::::::      :::   |||
Db       1006 ACGTTTGTGAGTCCTCAGCTGCTGAAATTGCTGATCTCCTTTGCAAGTGACCGTGAC--- 1062

Qy        126 MetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThr 145
                                 |||      |||      |||   :::|||
Db       1063 ---------ACATATTTGTGGATTGGATATCTCTGTGCAATCCTCTTATTCACTGCGGCT 1113

Qy        146 LeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCysAlaGlyMetArg 165
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Db       1114 CTCATTCAGTCTTTCTGCCTTCAGTGTTATTTCCAACTGTGCTTCAAGCTGGGTGTAAAA 1173

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Db       1174 GTACGGACAGCTATCATGGCTTCTGTATATAAGAAGGCATTGACCCTATCCAACTTGGCC 1233

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Db       1234 AGGAAGGAGTACACCGTTGGAGAAACAGTGAACCTGATGTCTGTGGATGCCCAGAAGCTC 1293

Qy        206 AspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIleAlaVal 225
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Qy        226 ThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaValLeuIle 245
                 ||||||   |||:::|||   |||   |||||||||:::   |||::::::
Db       1354 ATCTTCTTCCTATGGAGAGAGTTGGGACCCTCAGTCTTAGCAGGTGTTGGGGTGATGGTG 1413

Qy        246 IleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLysThr 265
              :::::::::|||:::   :::                     :::::::::   |||
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Qy        266 AlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIleArgIle 285
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              :::|||   :::|||||||||   ||||||   :::   :::   ||||||||||||
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Db       1594 GAGCTCAAGAACCTGCTGGCCTTTAGTCAACTACAGTGTGTAGTAATATTCGTCTTCCAG 1653

Qy        326 SerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeuGlySer--- 344
                       ::::::         |||||||||:::   |||||||||:::   |||
Db       1654 TTAACTCCAGTCCTGGTATCTGTGGTCACATTTTCTGTTTATGTCCTGGTGGATAGCAAC 1713

Qy        345 ---ValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValArgLeu 363
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Db       1714 AATATTTTGGATGCACAAAAGGCCTTCACCTCCATTACCCTCTTCAATATCCTGCGCTTT 1773

Qy        364 ThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIle 383
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Db       1774 CCCCTGAGCATG---CTTCCCATGATGATCTCCTCCATGCTCCAGGCCAGTGTTTCCACA 1830

Qy        384 ArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuPro 403
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Db       1831 GAGCGGCTAGAGAAGTACTTGGGAGGGGATGACTTGGACACATCTGCCATTCGACATGAC 1890

Qy        404 SerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSer 423
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Db       1951 GAAGCC---ACAGTCCGAGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2007

Qy        444 ValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAla 463

Db       2008 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2067

Qy        464 ProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrp 483
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Db       2068 NNNNNNNNNNNNNNNNNNNNNNNNNNNGGCACCACTGCCTATGTCCCACAGCAGTCCTGG 2127

Qy        484 ValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArg 503
              :::   :::||||||::::::   ||||||||||||||   ::::::   ::::::|||
Db       2128 ATTCAGAATGGCACCATAAAGGACAACATCCTTTTTGGAACAGAGTTTAATGAAAAGAGG 2187

Qy        504 TyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGly 523
              |||::::::|||::::::|||||||||      ||||||::::::|||      |||
Db       2188 TACCAGCAAGTACTGGAGGCCTGTGCTCTCCTCCCAGACTTGGAAATGCTGCCTGGAGGA 2247

Qy        524 AspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgVal 543
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Db       2248 GATTTGGCTGAGATTGGAGAGAAGGGTATAAATCTTAGTGGGGGTCAGAAGCAGCGGATC 2307
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Qy     544 AsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSer 563
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Qy     564 AlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln------Ile 581
Db    2368 GCAGTGGATGCTCATGTAGGAAAACATATTTTTAATAAGGTCTTGGGCCCCAATGGCCTG 2427

Qy     582 LeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSer 601
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Qy     602 GlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeu 621
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Qy     622 LysSerGlyIleAspPheGlySerLeuLeuLys------------------------- 632
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Qy     633 ---------------LysAspAsnGluGluSerGluGln--------------------- 640
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Qy     641 ---------------ProProValProGlyThrProThrLeuArg--------------- 650
Db    2668 AGTGTGGAAGAGATCCCCGAAGATGCAGCCTCCATAACCATGAGAAGAGAGAACAGCTTT 2727

Qy     651 AsnArgThrPheSerGluSerSerValTrpSer---------GlnGlnSerSerArgPro 667
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Qy     668 SerLeuLysAspGlyAlaLeuGluSer------GlnAspThrGluAsnVal------Pro 683
Db    2788 TCCTTGAAAACTCGGAATGTGAATAGCCTGAAGGAAGACGAAGAACTAGTGAAAGGACAA 2847

Qy     684 ValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLysAsn 703
Db    2848 AAACTAATTAAGAAGGAATTCATAGAAACTGGAAAGGTGAAGTTCTCCATCTACCTGGAG 2907

Qy     704 TyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAla 723
Db    2908 TACCTACAAGCAATAGGATTGTTTTCGATATTC---TTCATCATCCTTGCGTTTGTGATG 2964

Qy     724 AlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSer 743
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Qy     744 MetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsnTrp 763
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Qy     764 TyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSer 783
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Qy     797 LeuHisAsnLysMetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsn 816
Db    3166 TTGCACAAGCAACTGCTGAACAATATCCTTCGAGCACCTATGAGATTTTTTGACACAACA 3225

Qy     817 ProIleGlyArgIleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeu 836
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Qy     857 AlaValAlaValIleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIle 876
Db    3346 ATCTGCATGGCCACTCCTGTCTTCACCATCATCGTCATTCCTCTTGGCATTATTTATGTA 3405

Qy     877 PheLeuArgArgTyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThr 896
Db    3406 TCTGTTCAGATGTTTTATGTGTCTACCTCCCGCCAGCTGAGGCGTCTGGACTCTGTCACC 3465

Qy     897 ArgSerProValPheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAla 916
Db    3466 AGGTCCCCAATCTACTCTCACTTCAGCGAGACCGTATCAGGTTTGCCAGTTATCCGTGCC 3525

Qy     917 TyrLysAlaGluGluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGlu 936
Db    3526 TTTGAGCACCAGCAGCGATTTCTGAAACACAATGAGGTGAGGATTGACACCAACCAGAAA 3585

Qy     937 AlaTrpPheLeuPheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCys 956
Db    3586 TGTGTCTTTTCCTGGATCACCTCCAACAGGTGGCTTGCAATTCGCCTGGAGCTGGTTGGG 3645

Qy     957 AlaMetPheValIleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAla 976
Db    3646 AACCTGACTGTCTTCTTTTCAGCCTTGATGATGGTTATTTATAGAGATACCCTAAGTGGG 3705

Qy     977 GlyGlnValGlyLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCys 996
Db    3706 GACACTGTTGGCTTTGTTCTGTCCAATGCACTCAATATCACACAAACCCTGAACTGGCTG 3765

Qy     997 ValArgGlnSerAlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyr 1016
Db    3766 GTGAGGATGACATCAGAAATAGAGACCAACATTGTGGCTGTTGAGCGAATAACTGAGTAC 3825

Qy    1017 ThrAspLeuGluLysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpPro 1036
Db    3826 ACAAAAGTGGAAAATGAGGCACCCTGGGTGACTGATAAGAGGCCTCCGCCAGATTGGCCC 3885

Qy    1037 HisGluGlyValIleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeu 1056
Db    3886 AGCAAAGGCAAGATCCAGTTTAACAACTACCAAGTGCGGTACCGACCTGAGCTGGATCTG 3945

Qy    1057 ValLeuLysHisLeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArg 1076
Db    3946 GTCCTCAGAGGGATCACTTGTGACATTGGTAGCATGGAGAAGATTGGTGTGGTGGGCAGG 4005

Qy    1077 ThrGlyAlaGlyLysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGlu--- 1095
Db    4006 ACAGGAGCTGGAAAGTCATCCCTCACAAACTGCCTCTTCAGAATCTTAGAGGCTGCCGGT 4065

Qy    1096 GlyLysIleTrpIleAspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLys 1115
Db    4066 GGTCAGATTATCATTGATGGAGTAGATATTGCTTCCATTGGGCTCCACGACCTCCGAGAG 4125

Qy    1116 LysMetSerIleIleProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeu 1135
Db    4126 AAGCTGACCATCATCCCCCAGGACCCCATCCTGTTCTCTGGAAGCCTGAGGATGAATCTC 4185

Qy    1136 AspProPheAsnGluHisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeu 1155
Db    4186 GACCCTTTCAACAACTACTCAGATGAGGAGATTTGGAAGGCCTTGGAGCTGGCTCACCTC 4245

Qy    1156 LysGluThrIleGluAspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySer 1175
Db    4246 AAGTCTTTTGTGGCCAGCCTGCAACTTGGGTTATCCCACGAAGTGACAGAGGCTGGTGGC 4305

Qy    1176 AsnPheSerValGlyGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsn 1195
Db    4306 AACCTGAGCATAGGCCAGAGGCAGCTGCTGTGCCTGGGCAGGGCTCTGCTTCGGAAATCC 4365

Qy    1196 GlnIleLeuIleIleAspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIle 1215
Db    4366 AAGATCCTGGTCCTGGATGAGGCCACTGCTGCGGTGGATCTAGAGACAGACAACCTCATT 4425

Qy    1216 GlnLysLysIleArgGluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeu 1235
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Db          4426 CAGACGACCATCCAAAACGAGTTCGCCCACTGCACAGTGATCACCATCGCCCACAGGCTG 4485

Qy          1236 AsnThrIleIleAspSerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyr 1255
                 :::||||||:::|||||||||||:::||||||||||||:::|||::::::    |||
Db          4486 CACACCATCATGGACAGTGACAAGGTAATGGTCCTAGACAACGGGAAGATTATAGAGTGC 4545

Qy          1256 AspGluProTyrValLeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGln 1275
                       |||      |||||||||               ||||||   |||   ::::::
Db          4546 GGCAGCCCTGAAGAACTGCTACAA---ATCCCTGGACCCTTTTACTTTATGGCTAAGGAA 4602

Qy          1276 LeuGly 1277
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Db          4603 GCTGGC 4608
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RESULT 11
DQ038460

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LOCUS       DQ038460                4080 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Homo sapiens ABCC12 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ038460
VERSION     DQ038460.1  GI:66889669
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 4080)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 4080)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1..4080
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="16"
     gene            <1..>4080
                     /gene="ABCC12"
                     /locus_tag="HC8187"
ORIGIN

Alignment Scores:
Pred. No.:              9.58e-217      Length:        4080
Score:                  2043.50        Matches:       479
Percent Similarity:     54.7%          Conservative:  266
Best Local Similarity:  35.1%          Mismatches:    480
Query Match:            30.1%          Indels:        141
DB:                     11             Gaps:          27

US-09-976-858-42 (1-1325) x DQ038460 (1-4080)
```

```
Qy             1 MetLeuProVal------TyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeu 18
                 |||:::||||||               :::   |||||||||:::   ||||||   |||
Db            94 ATGATCCCAGTGCGACCCTGTGCAAGGTTAGCACCCAACCCGGTGGATGATGCCGGGCTA 153

Qy            19 CysSerArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArg 38
                    |||         |||   ||||||   |||:::         |||:::::::::|||
Db           154 CTCTCCTTCGCCACATTTTCCTGGCTCACGCCGGTGATGGTGAAAGGCTACCGGCAAAGG 213

Qy            39 LeuGluGluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGlu 58
                 |||      |||   :::      :::         |||   |||            :::
Db           214 CTGACCGTAGACACCCTGCCCCCATTGTCGACATATGACTCATCTGACACCAATGCCAAA 273

Qy            59 GluLeuGlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysPro 78
                    :::      ||||||:::||||||   |||                  :::|||
Db           274 AGATTTCGAGTCCTTTGGGATGAAGAGGTAGCAAGGGTG------GGTCCTGAGAAGGCC 327

Qy            79 SerLeuThrArgAlaIleIleLysCysTyrTrpLysSerTyr------------------ 92
                 ||||||:::         :::      ||||||
Db           328 TCTCTGAGCCACGTGGTG------------TGGAAATTCCAGAGGACACGCGTGTTGATG 375

Qy            93 ---LeuValLeuGlyIlePheThrLeuIleGluGluSerAlaLysValIleGlnProIle 111
                    :::|||      |||      :::|||         |||   :::         |||
Db           376 GACATCGTGGCCAACATCCTGTGCATCATC------ATGGCAGCCATAGGGCCGGTGATT 429

Qy           112 PheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspProMetAspSerValAlaLeu 131
                    :::   :::|||:::               |||               |||   :::
Db           430 CTCATTCACCAAATCCTCCAGCAGACTGAGAGGACCTCTGGGAAAGTCTGGGTTGGCATT 489

Qy           132 AsnThrAlaTyrAla---TyrAlaThrValLeuThr---------PheCysThrLeuIle 147
                             |||   :::||||||      |||            |||      |||
Db           490 GGACTGTGCATAGCCCTTTTTGCCACCGAGTTTACCAAAGTCTTCTTTTGGGCCCTTGCC 549

Qy           148 LeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCysAlaGlyMetArgLeuArg 167
                    ||||||   :::                                 :::||||||:::
Db           550 TGGGCCATCAACTACCGC------------------------ACGGCCATCCGGTTGAAG 585

Qy           168 ValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsnMetAlaMetGly 187
                 ||||||:::      :::::::::                     |||:::
Db           586 GTGGCGCTCTCCACCTTGGTTTTT------------------GAAAACCTAGTGTCCTTC 627

Qy           188 LysThrThrThr------------GlyGlnIleValAsnLeuLeuSerAsnAspValAsn 203
                 ||||||   |||               |||:::::::::|||:::||||||:::|||
Db           628 AAGACATTGACCCACATCTCTGTTGGCGAGGTGCTCAATATACTGTCAAGTGATAGCTAT 687

Qy           204 LysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIle 223
                          :::         :::|||                     |||:::      :::
Db           688 TCTTTGTTTGAAGCTGCCTTGTTTTGTCCTTTGCCAGCCACCATCCCGATCCTAATGGTC 747

Qy           224 AlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaVal 243
                          |||   :::         :::|||   |||   |||:::::::::|||
Db           748 TTTGTGCGGCGTACGCCTTTTTCATTCTGGGGCCCACAGCTCTCATCGGGATATCAGTG 807

Qy           244 LeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSer 263
                    :::|||   :::|||:::|||               ||||||   |||:::   |||
Db           808 TATGTCATATTCATACCCGTCCAGATGTTTATGGCCAAGCTCAATTCAGCTTTCCGAAGG 867

Qy           264 LysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIle 283
                                   ||||||   |||::::::||||||||||||   :::|||   |||
Db           868 TCAGCAATTTTGGTGACAGACAAGCGAGTTCAGACAATGAATGAGTTTCTGACCTGCATC 927

Qy           284 ArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArg 303
                 |||:::||||||||||||||||||||||||||||||:::|||      |||   ::::::|||
Db           928 AGGCTGATCAAAATGTATGCCTGGGAGAAATCTTTTACCAACACTATCCAAGATATAAGA 987

Qy           304 LysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAlaSer 323
                 ::::::|||                                    |||   |||
Db           988 AGGAGGGAAAGAAAATTACTGGAAAAAGCTGGATTTGTCCAAAGTGGAAACTCTGCCCTG 1047

Qy           324 PhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeuGly 343
                             |||   |||   :::   :::|||      :::   ::::::||||||
Db          1048 GCCCCCATCGTGTCCACCATAGCCATCGTGCTGACATTATCCTGCCACATCCTCCTGAGA 1107

Qy           344 SerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValArgLeu 363
                       :::||||||         |||      :::   ::::::      ::::::
Db          1108 CGCAAACTCACCGCACCCGTGGCATTTAGTGTGATTGCCATGTTTAATGTAATGAAGTTT 1167

Qy           364 ThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIle 383
                 ::::::   :::         |||   :::|||:::   ::::::||||||   ||||||:::
Db          1168 TCCATTGCAATC---TTGCCCTTCTCCATCAAAGCAATGGCTGAAGCGAATGTCTCTCTA 1224
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Qy    384 ArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuPro 403
Db   1225 AGGAGAATGAAGAAA---ATTCTCATAGATAAAAGCCCCCCATCTTACATCACCCAACCA 1281

Qy    404 SerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp---LysAla 422
Db   1282 GAAGACCCAGATACTGTCTTGCTTTTAGCAAATGCCACCTTGACATGGAGCATGAAGCC 1341

Qy    423 SerGluThrProThr------------------------------------------- 427
Db   1342 AGCAGGAAAAGTACCCCAAAGAAATTGCAGAACCAGAAAAGGCATTTATGCAAGAAACAG 1401

Qy    427 ------------------------------------------------------------ 427
Db   1402 AGGTCAGAGGCATACAGTGAGAGGAGTCCACCAGCCAAGGGAGCCACTGGCCCAGAGGAG 1461

Qy    428 -----------------------LeuGlnGlyLeuSerPheThrValArgProGlyGlu 439
Db   1462 CAAAGTGACAGCCTCAAATCGGTTCTGCACAGCATAAGCTTTGTGGTGAGAAAGGGGAAG 1521

Qy    440 LeuLeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeu 459
Db   1522 ATCTTGGGAATATGTGGGAATGTGGGAAGTGGAAAGAGCTCCCTCCTTGCAGCTCTCCTA 1581

Qy    460 GlyGluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSer 479
Db   1582 GGACAGATGCAGCTGCAGAAAGGGGTGGTGGCAGTCAATGGAACTTTGGCCTACGTTTCA 1641

Qy    480 GlnGlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyr 499
Db   1642 CAGCAGGCATGGATCTTTCATGGAAATGTGAGAGAAAACATACTCTTTGGAGAAAAGTAT 1701

Qy    500 GluLysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeu 519
Db   1702 GATCACCAAAGGTATCAGCACACAGTCCGCGTCTGTGGCCTCCAGAAGGACCTGAGCAAC 1761

Qy    520 LeuGluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGln 539
Db   1762 CTCCCCTATGGAGACCTGACTGAGATTGGGGAGCGGGGCCTCAACCTCTCTGGGGGGCAG 1821

Qy    540 LysAlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAsp 559
Db   1822 AGGCAGAGGATTAGCCTGGCCCGCGCTGTCTACTCCGACCGTCAGCTCTACCTGCTGGAC 1881

Qy    560 AspProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCys 579
Db   1882 GACCCCCTGTCGGCCGTGGACGCCCACGTGGGGAAGCACGTCTTTGAGGAGTGCATTAAG 1941

Qy    580 GlnIleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAla 599
Db   1942 AAGACGCTCAGGGGAAAGACAGTCGTCCTGGTGACCCACCAGCTACAGTTCTTAGAGTCT 2001

Qy    600 AlaSerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGlu 619
Db   2002 TGTGATGAAGTTATTTTATTAGAAGATGGAGAGATTTGTGAAAAGGGAACCCACAAGGAG 2061

Qy    620 PheLeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGlu------ 637
Db   2062 TTAATGGAG---------GAGAGAGGGCG-CTATGCAAAACTGATTCACAACCTGCGAGG 2111

Qy    638 -----------------------------------SerGluGlnProProValProGly 645
Db   2112 ATTGCAGTTCAAGGATCCTGAACACCTTTACAATGCAGCAATGGTGGAAGCCTTCAAGGA 2171

Qy    646 ThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGlnGlnSerSer 665
Db   2172 GAGCCCTG-CTGAGAGAGAGGAAGATGCTGGTATAATCGTTTTGGCTCCAGGAAATGAGA 2230

Qy    666 ArgProSerLeuLysAspGlyAlaLeuGluSerGln------AspThrGluAsnValPro 683
Db   2231 AAGATGAAGGA-AAAGAATCTGAAACAGGCTCAGAATTTGTAGACACAAAA---GTTCCT 2286

Qy    684 ------ValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyr 701
Db   2287 GAGCACCAGCTCATCCAGACTGAATCCCCCCAGGAAGGAACCGTGACCTGGAAAACATAT 2346

Qy    702 LysAsnTyrPheArgAlaGlyAlaHisTrpIle---------------ValPheIlePhe 716
Db   2347 CACACGTACATTAAGGCTTCTGGAGGGTACCTCCTTTCTCTCTTCACTGTGTTCCTCTTC 2406

Qy    717 LeuIleLeuLeuAsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSer 736
Db   2407 CTCCTGATGATTGGCAGCGCTGCC---------------TTCAGCAACTGGTGGCTGGGT 2451

Qy    737 TyrTrpAlaAsnLysGlnSerMetLeu------------------AsnValThrValAsn 750
Db   2452 CTCTGGTTGGACAAGGGCTCACGGATGACCTGTGGGCCCCAGGGCAACAGGACCATGTGT 2511

Qy    751 GlyGlyGlyAsnValThrGluLysLeuAspLeuAsnTrpTyrLeuGlyIleTyrSerGly 770
Db   2512 GAGGTCGGCGCGGTGCTGGCAGACATCGGTCAGCATGTGTACCAGTGGGTGTACACTGCA 2571

Qy    771 LeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeuValPheTyrValLeu 790
Db   2572 AGCATGGTGTTCATGCTGGTGTTTGGCGTCACCAAAGGCTTCGTCTTCACCAAGACCACA 2631

Qy    791 ValAsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIleLeuLysAlaProVal 810
Db   2632 CTGATGGCATCCTCCTCTCTGCATGACACGGTGTTTGATAAGATCTTAAAGAGCCCAATG 2691

Qy    811 LeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArgPheSerLysAspIleGly 830
Db   2692 AGTTTCTTTGACACGACTCCCACTGGCAGGCTAATGAACCGTTTTTCCAAGGATATGGAC 2751

Qy    831 HisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGlnThrLeuLeuGlnVal 850
Db   2752 GAGCTGGATGTGAGGCTGCCGTTTCACGCAGAGAACTTTCTGCAGCAGTTTTTATGGTG 2811

Qy    851 ValGlyValValSerValAlaValAlaValIleProTrpIleAlaIleProLeuValPro 870
Db   2812 GTGTTTATTCTCGTGATCTTGGCTGCTGTGTTTCCTGCTGTCCTTTTAGTCGTGGCCAGC 2871

Qy    871 LeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGluThrSerArgAspValLys 890
Db   2872 CTTGCTGTAGGCTTCTTCATTCTGTTACGCATTTTCCACAGAGGAGTCCAGGAGCTCAAG 2931

Qy    891 ArgLeuGluSerThrThrArgSerProValPheSerHisLeuSerSerSerLeuGlnGly 910
Db   2932 AAGGTGGAGAATGTCAGCCGGTCACCCTGGTTCACCCACATCACCTCCTCCATGCAGGGC 2991

Qy    911 LeuTrpThrIleArgAlaTyrLysAlaGluGluArgCysGlnGluLeuPheAspAlaHis 930
Db   2992 CTGGGCATCATTCACGCCTATGGCAAGAAGGAGAGCTGC---------ATCACCTATCAC 3042

Qy    931 GlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSerArgTrpPheAlaVal 950
Db   3043 --------------------CTCCTCTACTTTAACTGTGCTCTCAGGTGGTTTGCGCTG 3081

Qy    951 ArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPheGlySerLeuIleLeu 970
Db   3082 AGAATGGATGTCCTCATGAACATCCTTACCTTCACTGTGGCCTTGTTGGTGACCCTGAGT 3141

Qy    971 AlaLysThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyrAlaLeuThrLeuMet 990
Db   3142 TTCTCCTCCATCAGTACTTCATCCAAAGGCCTGTCATTGTCATACATCATCCAGCTGAGC 3201

Qy    991 GlyMetPheGlnTrpCysValArgGlnSerAlaGluValGluAsnMetMetIleSerVal 1010
Db   3202 GGACTGCTCCAAGTGTGTGTGCGAACGGGAACAGAGACGCAAGCCAAATTCACCTCCGTG 3261

Qy   1011 GluArgValIleGluTyrThrAspLeu---------GluLysGluAlaProTrpGluTyr 1027
Db   3262 GAGCTGCTCAGGGAATACATTTCGACCTGTGTTCCTGAATGCACTCATCCCCTCAAAGTG 3321

Qy   1028 GlnLysArgProProProAlaTrpProHisGluGlyValIleIlePheAspAsnValAsn 1047
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                 |||          ||||||       |||   |||   |||    :::
Db       3322 GGGACCTGTCCCAAGGAC---TGGCCCAGCTGTGGGAGATCACCTTCAGAGACTATCAG 3378

Qy       1048 PheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIleLysSer 1067
                    |||          |||||||||||       |||        |||:::|||
Db       3379 ATGAGATACAGAGACAACACCCCCCTTGTTCTCGACAGCCTGAACTTGAACATACAAAGT 3438

Qy       1068 GlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeuIleSerAla 1087
                 :::   ||||||||||||||||||||||||:::|||||||||||||||    |||
Db       3439 GGGCAGACAGTCGGGATTGTTGGAAGAACAGGTTCCGGAAAGTCATCGTTAGGAATGGCT 3498

Qy       1088 LeuPheArgLeuSerGluPro---GluGlyLysIleTrpIleAspLysIleLeuThrThr 1106
              ||||||||||||   ||||||      |||   |||:::||||||::::::
Db       3499 TTGTTTCGTCTGGTGGAGCCAGCCAGTGGCACAATCTTTATTGATGAGGTGGATATCTGC 3558

Qy       1107 GluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGluProValLeu 1126
                 :::   |||   |||||||||   |||:::::::::|||||||||:::|||||||||
Db       3559 ATTCTCAGCTTGGAAGACCTCAGAACCAAGCTGACTGTGATCCCACAGGATCCTGTCCTG 3618

Qy       1127 PheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThrAspGluGluLeu 1146
              |||   ||||||:::|||   |||||||||||||||      ||||||||||||   |||
Db       3619 TTTGTAGGTACAGTAAGGTACAACTTGGATCCCTTTGAGAGTCACACCGATGAGATGCTC 3678

Qy       1147 TrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLysMet 1166
              |||      |||:::            ::::::||||||         ||||||   |||:::
Db       3679 TGGCAGGTTCTGGAGAGAACATTCATGAGAGACACAATAATGAAACTCCCAGAAAAATTA 3738

Qy       1167 AspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGlnArgGlnLeuValCys 1186
                       |||:::   |||:::|||   |||||||||||||||:::|||||||||:::|||
Db       3739 CAGGCAGAAGTCACAGAAAATGGAGAAAACTTCTCAGTAGGGGAACGTCAGCTGCTTTGT 3798

Qy       1187 LeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAlaThrAlaAsn 1206
              :::||||||||||:::||||||   ::::::|||:::::::::||||||||||||||||:::
Db       3799 GTGGCCCGAGCTCTTCTCCGTAATTCAAAGATCATTCTCCTTGATGAAGCCACCGCCTCT 3858

Qy       1207 ValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPheAlaHisCys 1226
              :::|||   :::||||||   |||:::|||      |||:::::::   |||      |||
Db       3859 ATGGACTCCAAGACTGACACCCTGGTTCAGAACACCATCAAAGATGCCTTCAAGGGCTGC 3918

Qy       1227 ThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLysIleMetVal 1246
              ||||||||||||||||||||||||||||||||||:::::::::   |||      ::::::|||
Db       3919 ACTGTGCTGACCATCGCCCACCGCCTCAACACAGTTCTCAACTGCGATCACGTCCTGGTT 3978

Qy       1247 LeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGlnAsnLysGlu 1266
              :::::::::|||:::::::   |||:::|||:::|||   ||||||   :::      :::
Db       3979 ATGGAAAATGGGAAGGTGATTGAGTTTGACAAGCCTGAAGTCCTTGCAGAGAAGCCAGAT 4038

Qy       1267 SerLeuPhe 1269
              |||   |||
Db       4039 TCTGCATTT 4047
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RESULT 12
AY407265

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LOCUS       AY407265                4185 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Homo sapiens ABCC5 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY407265
VERSION     AY407265.1  GI:39763236
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 4185)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 4185)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1..>4185
                     /gene="ABCC5"
                     /locus_tag="HCM2833"
ORIGIN

Alignment Scores:
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Score:                  1968.50         Matches:         472
Percent Similarity:     51.4%           Conservative:    231
Best Local Similarity:  34.5%           Mismatches:      519
Query Match:            29.0%           Indels:          145
DB:                     10              Gaps:            28

US-09-976-858-42 (1-1325) x AY407265 (1-4185)

Qy         11 AsnProLeuGlnAspAlaAsnLeuCysSerArgValPhePheTrpTrpLeuAsnProLeu 30
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Db        166 CACCCAGTGGACAATGCTGGGCTTTTTCCTGTATGACTTTTCGTGGCTTTCTTCTCTG 225

Qy         31 PheLysIleGlyHisLysArg---ArgLeuGluGluAspAspMetTyrSerValLeuPro 49
                 ::::::   ||||||:::         |||      :::|||::::::|||:::
Db        226 GCCCGTGTGGCCCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAG 285

Qy         50 GluAspArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheTrpAspLysGluValLeu 69
                 :::   |||                     |||:::      |||   :::|||:::
Db        286 CACGAGTCTTCTGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAAT 345

Qy         70 ArgAlaGluAsnAspAlaGlnLysProSerLeuThrArgAlaIleIleLysCysTyrTrp 89
                          ||||||      :::      |||   ::::::      :::
Db        346 GAAGTTGGGCCAGACGCT---------GCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGC 396

Qy         90 LysSerTyrLeuValLeuGlyIlePheThrLeu---IleGluGluSerAlaLysValIle 108
              ::::::   |||:::|||   |||         |||   |||   :::   |||
Db        397 CGCACCAGGCTCATCCTGTCCATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGT 456

Qy        109 GlnProIlePheLeuGlyLys---IleIleAsnTyrPheGluAsnTyrAspProMetAsp 127
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Db        457 GGACCAGCCTTCATGGTGAAACACCTCTTGGAGTATACCCAG------------------ 498

Qy        128 SerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThrLeuIle 147
                    |||      :::         |||:::   :::|||            |||:::
Db        499 ------GCAACAGAGTCTAACCTGCAGTACAGCTTGTTGTTAGTGCTGGGCCTCCTCCTG 552

Qy        148 -----------------------LeuAlaIleLeuHisHisLeuTyrPheTyrHisVal 159
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Db        553 ACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGGGCATTGAATTACCGA------ 606

Qy        160 GlnCysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeu 179
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Db        607 ------ACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAGAAGATCCTT 660

Qy        180 ArgLeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSer 199
              :::|||   |||:::            :::   :::   |||:::::::::|||:::   |||
Db        661 AAGTTAAAGAACATTAAA------GAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCC 714

Qy        200 AsnAspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyPro 219
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Db        715 AACGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGACCC 774
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Qy     220 LeuGlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAla 239
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Qy     240 GlyMetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSer 259
Db     835 GGATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACAGCA 894

Qy     260 SerLeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluVal 279
Db     895 TATTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAAGTT 954

Qy     280 IleThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIle 299
Db     955 CTTACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGTGTT 1014

Qy     300 ThrAsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMet 319
Db    1015 CAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1074

Qy     320 AsnLeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyr 339
Db    1075 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1134

Qy     340 ValLeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGly 359
Db    1135 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGCTTTCACAGTGGTGACAGTCTTCAAT 1194

Qy     360 AlaVal------ArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSer 377
Db    1195 TCCATGACTTTTGCTTTGAAAGTAACA---------CCGTTTTCAGTAAAGTCCCTCTCA 1245

Qy     378 GluAlaIleValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGln 397
Db    1246 GAAGCCTCAGTGGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATG 1305

Qy     398 ---ArgAsnArgGlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThr 416
Db    1306 ATAAAGAACAAA------CCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACC 1359

Qy     417 AlaPheTrpAspLys------------------------------------------- 421
Db    1360 TTGGCATGGGACTCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATG 1419

Qy     421 ------------------------------------------------------------ 421
Db    1420 AAAAAAGACAAGAGGGCTTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACT 1479

Qy     422 ------------------------------------------------AlaSerGluThr 425
Db    1480 GAGCATCAGGCGGTGCTGGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGG 1539

Qy     426 Pro--------------------------------------------------------- 426
Db    1540 CCCAGTCCCGAAGAGGAAGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGG 1599

Qy     427 ThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGlyPro 446
Db    1600 ACACTGCACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGTGGCAGT 1659

Qy     447 ValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHis 466
Db    1660 GTGGGAAGTGGAAAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAG 1719

Qy     467 GlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPheSer 486
Db    1720 GGCAGCATTGCAATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAAT 1779

Qy     487 GlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGluLys 506
Db    1780 GCTACTCTGAGAGACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCT 1839

Qy     507 ValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThr 526
Db    1840 GTGCTGAACAGCTGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACG 1899

Qy     527 ValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAla 546
Db    1900 GAGATTGGAGAGCGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCC 1959

Qy     547 ArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAsp 566
Db    1960 CGGGCCTTGTATAGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGAT 2019

Qy     567 AlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeuHisGluLysIle 586
Db    2020 GCCCATGTGGGCAACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACA 2079

Qy     587 ThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIleLeu 606
Db    2080 GTTCTGTTTGTTACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATG 2139

Qy     607 LysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIleAsp 626
Db    2140 AAAGAGGGCTGTATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGAC 2199

Qy     627 ------------PheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProPro 642
Db    2200 TATGCTACCATTTTTAATAACCTGTTGCTG---------------GGAGAGACACCGCCA 2244

Qy     643 ValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGln 662
Db    2245 GTTGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2304

Qy     663 GlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnVal 682
Db    2305 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGCAGCTTGTG 2364

Qy     683 ProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLys 702
Db    2365 CAGCTG------------GAAGAGAAAGGGCAGGGTTCAGTGCCCTGGTCAGTATATGGT 2412

Qy     703 AsnTyrPheArgAlaGlyAla---------HisTrpIleValPheIlePheLeuIleLeu 719
Db    2413 GTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTGGTTATTATGGCCCTTTTCATG 2472

Qy     720 LeuAsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAla 739
Db    2473 CTGAATGTAGGCAGCACC---------GCCTTCAGCACCTGGTGGTTGAGTTACTGGATC 2523

Qy     740 AsnLysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeu 759
Db    2524 ---AAGCAAGGAAGCGGGAACACCACTGTGACT---CGAGGGAACGAGACCTCGGTGAGT 2577

Qy     760 Asp---------------------LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThr 772
Db    2578 GACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTCTCCATG 2637

Qy     773 ValAlaThrValLeuPheGlyIleAlaArgSerLeuLeuValPheTyrValLeuValAsn 792
Db    2638 GCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGCGA 2697

Qy     793 SerSerGlnThrLeuHisAsnLysMetPheGluSerIleLeuLysAlaProValLeuPhe 812
Db    2698 GCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAAGTTT 2757

Qy     813 PheAspArgAsnProIleGlyArgIleLeuAsnArgPheSerLysAspIleGlyHisLeu 832
Db    2758 TTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTT 2817

Qy     833 AspAspLeuLeuProLeuThrPheLeuAspPheIleGlnThrLeuLeuGlnValValGly 852
Db    2818 GACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTGTTCTTC 2877

Qy     853 ValValSerValAlaValAlaValIleProTrpIleAlaIleProLeuValProLeuGly 872
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Db      2878 TGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCCTTGTC 2937

Qy       873 IleIlePheIlePheLeuArgArgTyrPheLeuGluThrSerArgAspValLysArgLeu 892
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Db      2938 ATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAGCGTCTG 2997

Qy       893 GluSerThrThrArgSerProValPheSerHisLeuSerSerSerLeuGlnGlyLeuTrp 912
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Db      2998 GACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGCCTTGCC 3057

Qy       913 ThrIleArgAlaTyr---LysAlaGluGlu---------ArgCysGlnGluLeuPheAsp 928
             ||||||   ||||||   |||    :::|||         |||   |||||||||    |||
Db      3058 ACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGAT 3117

Qy       929 AlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSerArgTrpPhe 948
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Db      3118 GACAACCAA------------GCTCCTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTG 3165

Qy       949 AlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPheGlySerLeu 968
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Db      3166 GCTGTGCGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTT 3225

Qy       969 IleLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyrAlaLeuThr 988
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Db      3226 CTTATGCACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAG 3285

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Db      3286 TTAACGGGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACC 3345

Qy      1009 SerValGluArgValIleGluTyr---ThrAspLeuGluLysGluAlaProTrpGluTyr 1027
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Db      3346 TCGGTGGAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATT 3405

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Db      3406 AAGAACAAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCA 3465

Qy      1047 AsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIleLys 1066
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Db      3466 GAGATGAGGTACCGAGAAAACCTCCCTCTCGTCCTAAAGAAAGTATCCTTCACGATCAAA 3525

Qy      1067 SerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeuIleSer 1086
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Db      3526 CCTAAAGAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATG 3585

Qy      1087 AlaLeuPheArgLeuSerGluProGluGlyLys---IleTrpIleAspLysIleLeuThr 1105
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Db      3586 GCCCTCTTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATC 3645

Qy      1106 ThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGluProVal 1125
             ::::::||||||||||   ||||||||||   |||:::||||||||||||||||||||||||
Db      3646 AGTGATATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTG 3705

Qy      1126 LeuPheThrGlyTyrMetArgLysAsnLeuAspProPheAsnGluHisThrAspGluGlu 1145
             ||||||:::||||||:::|||   |||||||||||||||||::::::|||:::::::::
Db      3706 CTGTTCAGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAG 3765

Qy      1146 LeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLys 1165
             :::|||:::||||||:::            :::||||||   |||      ||||||   |||
Db      3766 ATTTGGGATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAA 3825

Qy      1166 MetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGlnArgGlnLeuVal 1185
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Db      3826 CTTGAATCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTG 3885

Qy      1186 CysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAlaThrAla 1205
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Db      3886 TGCATAGCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCT 3945

Qy      1206 AsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPheAlaHis 1225
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Db      3946 GCCATGGACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGAC 4005

Qy      1226 CysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLysIleMet 1245
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Db      4006 TGTACCATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATG 4065

Qy      1246 ValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGlnAsnLys 1265
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Db      4066 GTGCTGGCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGAC 4125

Qy      1266 GluSerLeuPheTyrLysMet 1272
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RESULT 13
AY407267

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LOCUS       AY407267                4176 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus ABCC5 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY407267
VERSION     AY407267.1  GI:39763238
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4176)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 4176)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              4.64e-207      Length:         4176
Score:                  1957.50        Matches:        469
Percent Similarity:     51.7%          Conservative:   235
Best Local Similarity:  34.4%          Mismatches:     522
Query Match:            28.8%          Indels:         137
DB:                     10             Gaps:           26

US-09-976-858-42 (1-1325) x AY407267 (1-4176)

Qy        11 AsnProLeuGlnAspAlaAsnLeuCysSerArgValPhePheTrpTrpLeuAsnProLeu 30
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Db       157 CACCCAGTGGACAATGCTGGACTTTTCTCCTACATGACCTTTTCATGGCTCTCTCCTCTG 216

Qy        31 PheLysIleGlyHisLysArg---ArgLeuGluGluAspAspMetTyrSerValLeuPro 49
                ::::::   ||||||:::         |||      :::|||::::::   :::
Db       217 GCCCGAGTGGTTCACAAGAAGGGGGAGCTGTTAATGGAGGATGTGTGGCCTTTGTCCAAG 276
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Qy          50 GluAspArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheTrpAspLysGluValLeu 69
Db         277 TATGAGTCTTCTGATGTGAACAGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAAT 336

Qy          70 ArgAlaGluAsnAspAlaGlnLysProSerLeuThrArgAlaIleIleLysCysTyrTrp 89
Db         337 GAAGTTGGGCCAGACGCT---------GCCTCCCTGCGAAGGGTTGTGTGGATCTTTTGC 387

Qy          90 LysSerTyrLeuValLeuGlyIlePheThrLeu---IleGluGluSerAlaLysValIle 108
Db         388 CGCACCAGGCTCATCCTGTCCATCGTGTGCCTGATGATCACGCAGTTGGCTGGCTTCAGT 447

Qy         109 GlnProIlePheLeuGlyLys---IleIleAsnTyrPheGluAsnTyrAspProMetAsp 127
Db         448 GGACCAGCCTTCGTGGTGAAGCACCTCTTGGAGTACACCCAG------------------ 489

Qy         128 SerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThrLeuIle 147
Db         490 ------GCAACAGAGTCTAACCTGCAGTACAGCTTGCTGTTAGTGTTAGGCCTACTCCTG 543

Qy         148 ------------------------LeuAlaIleLeuHisHisLeuTyrPheTyrHisVal 159
Db         544 ACAGAAGTTGTACGCTCCTGGTCACTTGCACTGACTTGGGCATTGAATTATCGA------ 597

Qy         160 GlnCysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeu 179
Db         598 ------ACTGGTGTCCGGTTGCGGGGGGCTATCCTGACTATGGCATTCAAGAAGATCCTG 651

Qy         180 ArgLeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSer 199
Db         652 AAGTTAAAGAACATTAAA------GAAAAGTCCCTAGGGGAGCTCATCAATATCTGCTCC 705

Qy         200 AsnAspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyPro 219
Db         706 AATGATGGGCAAAGGATGTTTGAGGCAGCCGCTGTGGGCAGCTTGCTGGCTGGAGGACCT 765

Qy         220 LeuGlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAla 239
Db         766 GTTGTTGCCATCTTGGGCATGATTTATAATGTAATCATCCTAGGACCCACGGGCTTCCTG 825

Qy         240 GlyMetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSer 259
Db         826 GGATCAGCGGTTTTTATCCTCTTTTATCCAGCAATGATGTTCGTGTCACGGCTAACTGCA 885

Qy         260 SerLeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluVal 279
Db         886 TATTTCAGGAGAAAGTGTGTAGCTGCCACAGATGACCGTGTCCAGAAGATGAATGAAGTT 945

Qy         280 IleThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIle 299
Db         946 CTTACCTACATTAAATTCATTAAAATGTATGCCTGGGTCAAAGCGTTTTCTCAGTGTGTG 1005

Qy         300 ThrAsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMet 319
Db        1006 CAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1065

Qy         320 AsnLeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyr 339
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Qy         340 ValLeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGly 359
Db        1126 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGCCTTCACAGTGGTGACTGTCTTCAAT 1185

Qy         360 AlaVal------ArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSer 377
Db        1186 TCCATGACTTTTGCTTTAAAAGTAACA---------CCATTCTCAGTGAAGTCCCTCTCT 1236

Qy         378 GluAlaIleValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGln 397
Db        1237 GAAGCATCAGTGGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATG 1296

Qy         398 ---ArgAsnArgGlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThr 416
Db        1297 ATAAAGAACAAA------CCGGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACC 1350

Qy         417 AlaPheTrpAspLys--------------------------------------------- 421
Db        1351 TTGGCATGGGACTCCTCCCACTCCAGTATACAGAACTCGCCCAAGCTGACCCCCAAAATG 1410

Qy         421 ------------------------------------------------------------ 421
Db        1411 AAAAAAGACAAGAGGGCTACCAGGGGCAAGAAAGAGAAGTCGAGGCAGCTGCAACACACT 1470

Qy         422 ------------------------------------------------AlaSerGluThr 425
Db        1471 GAGCACCAGGCGGTGCTGGCAGAACAGAAAGGACACCTCCTCCTGGACAGTGACGAGCGG 1530

Qy         426 Pro--------------------------------------------------------- 426
Db        1531 CCCAGCCCGGAAGAGGAAGAAGGCAAGCAGATCCACACAGGGAGCCTGCGCCTGCAGAGG 1590

Qy         427 ThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGlyPro 446
Db        1591 ACACTGTACAACATTGACTTAGAAATTGAAGAGGGCAAACTGGTTGGAATCTGCGGCAGT 1650

Qy         447 ValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHis 466
Db        1651 GTGGGAAGTGGAAAAACCTCTCTCGTTTCAGCCATTTTAGGCCAGATGACGCTTTTGGAG 1710

Qy         467 GlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPheSer 486
Db        1711 GGCAGCATTGCCGTCAGTGGGACCTTTGCTTATGTGGCCCAACAGGCCTGGATTCTCAAT 1770

Qy         487 GlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGluLys 506
Db        1771 GCCACTCTGAGAGACAACATTCTCTTTGGGAAGGAATTTGATGAAGAGAGATACAACTCA 1830

Qy         507 ValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThr 526
Db        1831 GTGCTGAATAGCTGCTGCCTGCGGCCTGACTTGGCCATTCTCCCCAACAGCGACCTGACT 1890

Qy         527 ValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAla 546
Db        1891 GAGATTGGAGAGCGAGGAGCCAACCTGAGTGGTGGACAGCGCCAGAGAATCAGCCTTGCT 1950

Qy         547 ArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAsp 566
Db        1951 AGAGCCTTGTACAGTGATAGAAGCATCTACATCCTGGATGACCCCCTCAGTGCCTTAGAT 2010

Qy         567 AlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeuHisGluLysIle 586
Db        2011 GCCCATGTGGGCAACCACATCTTCAACAGTGCTATCCGGAAGCGCCTCAAGTCTAAGACG 2070

Qy         587 ThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIleLeu 606
Db        2071 GTTCTGTTTGTTACACACCAGTTACAGTATCTGGTCGATTGTGATGAGGTGATCTTCATG 2130

Qy         607 LysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIleAsp 626
Db        2131 AAGGAAGGCTGTATCACAGAGAGAGGTACCCATGAGGAGCTGATGAACTTAAATGGGGAT 2190

Qy         627 ------------PheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProPro 642
Db        2191 TACGCTACGATTTTTAATAACCTGTTGCTG---------------GGAGAGACACCCCCA 2235

Qy         643 ValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGln 662
Db        2236 GTTGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2295

Qy         663 GlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnVal 682
Db        2296 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGCAGCTTGTG 2355

Qy         683 ProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLys 702
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Db       2356 CAGGTG------------GAGGAGAAAGGGCAAGGTTCTGTGCCTTGGTCAGTCTACTGG 2403

Qy        703 AsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThr 722
                 |||  :::|||               :::   |||:::   :::::::::|||
Db       2404 GTCTACATCCAGGCTGCAGGGGGCCCCTTGGCTTTCCTGGTCATCATGGTCCTCTTCATG 2463

Qy        723 AlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGln 742
                          :::                |||||||||||||||||||   ||||||
Db       2464 CTGAATGTGGGCAGCACTGCCTTCAGCACCTGGTGGCTTAGCTACTGGATC---AAGCAA 2520

Qy        743 SerMetLeuAsnValThrValAsnGlyGlyGlyAsn------ValThrGluLysLeuAsp 760
                          |||  ||||||     |||              |||::::::   :::
Db       2521 GGAAGCGGGAACAGCACAGTGTATCAAGGGAACAGAAGCTTCGTGAGTGACAGCATGAAG 2580

Qy        761 ------------LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrVal 776
                          :::   :::|||      ||||||:::                   :::
Db       2581 GACAACCCCTTCATGCAGTACTACGCCAGCATCTACGCCCTCTCCATGGCAGTCATGCTG 2640

Qy        777 LeuPheGlyIleAlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThr 796
              :::               |||   ::::::               :::   :::|||
Db       2641 ATCTTGAAAGCCATTCGAGGAGTTGTCTTCGTCAAGGGCACACTGAGAGCCTCCTCCCGG 2700

Qy        797 LeuHisAsnLysMetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsn 816
              ||||||:::::::::|||      ||||||:::   :::   |||||||||
Db       2701 CTCCATGATGAGCTATTCCGAAGGATCCTTAGGAGCCCCATGAAGTTTTTGATACTACC 2760

Qy        817 ProIleGlyArgIleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeu 836
               |||   ||||||||||||||||||||||||||||||:::      :::|||      |||
Db       2761 CCAACAGGAAGGATTCTCAACAGGTTTTCCAAAGACATGGATGAAGTGGATGTGCGGCTG 2820

Qy        837 ProLeuThrPheLeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerVal 856
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Qy        857 AlaValAlaValIleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIle 876
                       |||   ||||||      :::   :::   ||||||   |||:::|||
Db       2881 ATTGCTGGAGTCTTCCCATGGTTCCTCGTGGCGGTGGGGCCTCTCCTCATCCTCTTCTCA 2940

Qy        877 PheLeuArgArgTyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThr 896
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Db       2941 CTTCTCCACATTGTCTCCAGGGTCCTGATTCGTGAGCTAAAGCGGTTGGACAATATCACG 3000

Qy        897 ArgSerProValPheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAla 916
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Db       3001 CAGTCTCCTTTCCTCTCCCACATCACGTCTAGCATTCAGGGCCTGGCCACCATCCATGCC 3060

Qy        917 Tyr---LysAlaGluGlu---------ArgCysGlnGluLeuPheAspAlaHisGlnAsp 932
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Db       3061 TACAACAAAAGGCAGGAGTTTTACACAGGTATCAGGAGCTCCTGGATGACAACCAG--- 3117

Qy        933 LeuHisSerGluAlaTrpPheLeuPheLeuThrThrSerArgTrpPheAlaValArgLeu 952
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Db       3118 ---------GCTCCCTTTTTCCTGTTCACCTGTGCAATGAGGTGGCTGGCAGTGCGGCTG 3168

Qy        953 AspAlaIleCysAlaMetPheValIleIleValAlaPheGlySerLeuIleLeuAlaLys 972
              |||   |||                  :::                  :::::::::
Db       3169 GACCTCATCAGCATTGCCCTGATTACCACCACTGGCCTGATGATTGTTCTCATGCATGGA 3228

Qy        973 ThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMet 992
                 :::   :::            ||||||||:::|||||||||:::   |||   |||:::
Db       3229 CAGATCCCTTCAGCCTATGCGGGGCTTGCCATCTCCTACGCTGTGCAGTTAACTGGACTA 3288

Qy        993 PheGlnTrpCysValArgGlnSerAlaGluValGluAsnMetMetIleSerValGluArg 1012
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Db       3289 TTCCAGTTCACCGTCAGACTGGCATCGGAGACAGAAGCACGGTTCACTTCCGTGGAGAGG 3348

Qy       1013 ValIleGluTyr---ThrAspLeuGluLysGluAlaProTrpGluTyrGln---LysArg 1030
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Db       3349 ATCAACCACTATATCAAGACTCTCTCTTTGGAAGCACCTGCCAGAATCAAGAACAAGGCT 3408

Qy       1031 ProProProAlaTrpProHisGluGlyValIleIlePheAspAsnValAsnPheMetTyr 1050
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Db       3409 CCTCCCCATGACTGGCCCCAGGAGGGAGAAGTAACCTTTGAGAATGCAGAAATGAGATAC 3468

Qy       1051 SerProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIleLysSerGlnGluLys 1070
                                       ||||||||||||||   ::::::      ||||||   :::||||||
Db       3469 CGGGAAAATCTCCCTCTGGTCCTTAAGAAAGTGTCCTTCACCATCAAGCCCAAGGAAAAG 3528

Qy       1071 ValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeuIleSerAlaLeuPheArg 1090
              :::||||||||||||||||||||||:::||||||||||||||||         ||||||||||||
Db       3529 ATAGGCATTGTGGGACGAACAGGGTCAGGGAAGTCCTCTTTGGGGATGGCCCTCTTCCGT 3588

Qy       1091 LeuSerGluProGluGlyLys---IleTrpIleAspLysIleLeuThrThrGluIleGly 1109
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Db       3589 CTGGTGGAGCTATCTGGAGGCTGCATCAAGATTGATGGAATAAGAATCAGTGACATCGGC 3648

Qy       1110 LeuHisAspLeuArgLysLysMetSerIleIleProGlnGluProValLeuPheThrGly 1129
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Db       3649 CTGGCCGACCTCCGAAGCAAACTGGCCATCATTCCTCAGGAGCCAGTGCTGTTCAGTGGC 3708

Qy       1130 ThrMetArgLysAsnLeuAspProPheAsnGluHisThrAspGluGluLeuTrpAsnAla 1149
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Db       3709 ACTGTCAGATCAAACCTGGACCCTTTCAACCAGTACACGGAAGACCAGATCTGGGATGCT 3768

Qy       1150 LeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLysMetAspThrGlu 1169
              |||:::         :::||||||   |||      ||||||   |||:::::::::|||
Db       3769 CTAGAGAGAACGCACATGAAGGAATGTATTGCCCAGCTACCTCTGAAACTTGAGTCTGAA 3828

Qy       1170 LeuAlaGluSerGlySerAsnPheSerValGlyGlnArgGlnLeuValCysLeuAlaArg 1189
              :::      |||:::|||   ||||||||||||||||||:::|||||||||:::|||:::||||||
Db       3829 GTAATGGAGAACGGGGACAACTTCTCTGTTGGGGAACGGCAGCTGTTGTGCATAGCAAGA 3888

Qy       1190 AlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAlaThrAlaAsnValAspPro 1209
              |||:::||||||         :::|||||||||:::||||||||||||||   :::|||
Db       3889 GCCCTGCTGCGTCACTGTAAGATTCTGATTTTAGATGAAGCTACAGCCGCTATGGACACA 3948

Qy       1210 ArgThrAspGluLeuIleGlnLysLysIleArgGluLysPheAlaHisCysThrValLeu 1229
                 ||||||   |||||||||:::   |||||||||   ||||||   ||||||:::|||
Db       3949 GAGACAGACTTACTGATCCAGGAGACCATCCGGGAAGCATTTGCGGACTGCACCATGCTG 4008

Qy       1230 ThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLysIleMetValLeuAspSer 1249
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Db       4009 ACCATTGCCCATCGCCTGCACACAGTTCTGGGCTCTGACAGGATCATGGTGCTGGCCCAG 4068

Qy       1250 GlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGlnAsnLysGluSerLeuPhe 1269
              |||::::::   |||:::|||   |||   |||||||||   |||         |||   |||
Db       4069 GGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCTAATGACAGTTCAAGATTC 4128

Qy       1270 TyrLysMet 1272
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Db       4129 TATGCCATG 4137
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RESULT 14
CL957124

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LOCUS       CL957124                4483 bp    DNA     linear   GSS 21-SEP-2004
DEFINITION  OsJRUA001445 Oryza sativa Express Library Oryza sativa (indica
            cultivar-group) genomic, genomic survey sequence.
ACCESSION   CL957124
VERSION     CL957124.1  GI:52369499
KEYWORDS    GSS.
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 4483)
  AUTHORS   Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
            Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
            Wong,G.K.S., Deng,X.W. and Wang,J.
  TITLE     An analysis of transcriptional regulation of the rice genome and
            its comparison to Arabidopsis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Chen Chen
            Department of Bioinformatic
            Beijing Institute of Genomics
```

```
          Chinese Academy of Sciences, Beijing 101300, China
          Tel: 86-10-80481559
          Fax: 86-10-80488676
          Email: chenchen@genomics.org.cn
          Rice genomic sequence.
          Class: exon-trapped.
FEATURES             Location/Qualifiers
     source          1..4483
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:39946"
                     /clone_lib="Oryza sativa Express Library"
                     /note="Oryza sativa exon trapped genomic sequences "
ORIGIN

Alignment Scores:
Pred. No.:              1.01e-206      Length:         4483
Score:                  1955.00        Matches:        442
Percent Similarity:     54.8%          Conservative:   263
Best Local Similarity:  34.4%          Mismatches:     524
Query Match:            28.8%          Indels:         57
DB:                     10             Gaps:           19

US-09-976-858-42 (1-1325) x CL957124 (1-4483)

Qy         16 AlaAsnLeuCysSerArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHis 35
              |||        |||   :::  |||   |||:::  |||||      :::||||||
Db        694 GCCGGCTTCCTCAGCGTCCTCACCTTCTCGTGGATGGTCCCCTCCTCGCCGTCGGACAC 753

Qy         36 LysArgArgLeuGluGluAspAspMetTyrSerValLeuProGluAspArgSerGlnHis 55
              ::::::    |||:::    ||||||:::        :::    |||    |||||
Db        754 AGGAAGACCCTCGACCTCGACGACGTCCCGGGCCTCGACCCCGGCGACAGAGTCGCCGGT 813

Qy         56 LeuGlyGluGluLeuGlnGlyPhe---TrpAspLysGluValLeuArgAlaGluAsnAsp 74
              |||      |||   |||            :::    |||   |||       :::
Db        814 CTG---------CTCCCGCCGTTCAAGACCAACCTCGAGGCGCTCGCCGGCGACGGCTCT 864

Qy         75 AlaGlnLysPro---------SerLeuThrArgAlaIleIleLysCysTyrTrpLysSer 91
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Db        865 GGGCGGAAGGTCACGGCGTTCACGCTCTCCAAGGCACTGGTGCGCACCGTGTGGTGGCAC 924

Qy         92 TyrLeuValLeuGlyIlePheThrLeuIleGluGluSerAlaLysValIleGlnProIle 111
                       |||          :::   |||:::          :::      :::   |||
Db        925 GTCGCGGTGACCGCGTTCTACGCGCTGGTCTACAACGTCTCCACCTACGTCGGCCCTTAC 984

Qy        112 PheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspProMetAspSerValAlaLeu 131
                 :::    ::::::   |||                                    |||
Db        985 CTCATCGACTCGCTCGTGCAATAC---------------------------------CTC 1011

Qy        132 AsnThrAlaTyrAlaTyrAlaThr---------ValLeuThrPheCysThrLeuIleLeu 148
              |||            ||||||:::              :::|||           ::::::
Db       1012 AACGGCGACGAGAGGTACGCGAGCAAGGGGCAGCTGCTTGTCCTTGCCTTCATCGTCGCC 1071

Qy        149 AlaIleLeuHisHisLeu------------TyrPheTyrHisValGlnCysAlaGlyMet 164
                 :::         |||                  :::|||:::    :::|||     ||||||:::
Db       1072 AAGGTGTTCGAGTGTTTGTCCCAACGGCACTGGTTCTTCCGGCTGCAGCAGGCCGGGATA 1131

Qy        165 ArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsnMet 184
              |||   |||   |||:::            ::::::|||:::|||   |||      ||||||:::
Db       1132 CGCGCGCGGTCGGCGCTCGTCGCCGTCGTCTACCAGAAGGGGCTCGTGCTGTCTAGCCAA 1191

Qy        185 AlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsnLys 204
              :::                |||:::|||:::::::::|||::::::|||    |||      ::::::
Db       1192 TCCAGGCAGAGCCGCACGAGCGGCGAGATGATCAACATCATCAGCGTCGACGCCGACCGC 1251

Qy        205 PheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIleAla 224
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Db       1252 GTCGGCCTCTTCTCGTGGTACATGCACGACCTCTGGTTGGTGCCACTCCAAGTAGGCATG 1311

Qy        225 ValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaValLeu 244
                       :::|||:::          :::|||::::::    ||||||          :::
Db       1312 GCATTGTTCATCCTGTACTCCACCCTTGGGCTTGCCTCGCTTGCTGCGCTTGGTGCCACT 1371

Qy        245 IleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLys 264
              ::::::::::::                        |||::::::                 :::   |||
Db       1372 GTTGTTGTCATGCTTGCCAATGTGCCTCCAGGGCAAATGCAGGAAAAGTTCCAGCAGAAG 1431

Qy        265 ThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIleArg 284
                             |||   |||::::::             :::|||::::::      :::|||
Db       1432 CTGATGGACTGCAAGGATGTCAGGATGAAAGCAACATCTGAGATCCTACGCAACATGAGG 1491

Qy        285 IleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArgLys 304
              |||:::|||:::       ||||||          |||      :::      |||      :::|||||||||
Db       1492 ATTCTTAAATTGCAGGGGTGGGAGATGAAGTTCTTGTCCAAGATCATCGACCTGAGGAAG 1551

Qy        305 LysGlu---------IleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeu 321
                 |||              :::   |||   |||      :::|||   :::
Db       1552 ACGGAGACAAACTGGCTCAAGAAATATCTCTACACATCGACCATTGTTACCTTT------ 1605

Qy        322 AlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeu 341
                    |||:::   |||                :::      |||||||||         :::|||
Db       1606 ---GTGTTCTGGGGAGCCCCAACATTTGTGGCAGTGGTGACCTTCATAGCTTGCATGCTC 1662

Qy        342 LeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaVal 361
              :::|||         :::      :::      :::|||             |||:::             :::       :::
Db       1663 ATGGGGATACCATTGGAGTCAGGGAAGGTGCTATCTGCACTGGCCACATTCCGCGTGCTG 1722

Qy        362 ArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleVal 381
              :::         :::                  |||         :::      :::      |||
Db       1723 CAAGAACCGATA---TACAATCTTCCCGACACGATCTCAATGTTGATTCAGACCAAGGTG 1779

Qy        382 SerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIle---SerGlnArgAsnArg 400
              |||:::   ||||||      :::||||||      |||:::|||:::         :::
Db       1780 TCTCTTGACAGGATAGCATCCTTTTTATGCCTCGAGGAATTGCCGACTGATGCTGTGCTG 1839

Qy        401 GlnLeuProSerAspGlyLysLysMet---ValHisValGlnAspPheThrAlaPheTrp 419
              :::|||||||||                     :::      :::      |||::::::                  |||
Db       1840 AAACTTCCAAGTGGTAGCTCAGATGTTGCAATTGAGGTCAGAAATGGGTGCTTTTCTTGG 1899

Qy        420 AspLysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGlu 439
              |||      :::      |||      |||||||||:::      |||:::|||            :::   |||
Db       1900 GATGCCTCACCTGAAGTGCCAACGTTGAAGGATCTGAACTTTCAAGCTCAACAAGGTATG 1959

Qy        440 LeuLeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeu 459
                 :::||||||   |||   |||      ||||||||||||||||||||||||         :::|||
Db       1960 CGTATTGCAGTCTGTGGGACTGTCGGCTCTGGAAAATCAAGCTTGTTGTCTTGCATTCTT 2019

Qy        460 GlyGluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSer 479
              ||||||:::                  |||      |||               |||      :::||||||||||||
Db       2020 GGTGAGATTCCAAAGCTATCAGGAGAGGTCAAGACCTGTGGGACGATGGCGTATGTGAGC 2079

Qy        480 GlnGlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyr 499
              |||      |||:::      ||||||         ::::::      ||||||||||||||||||:::
Db       2080 CAGTCGGCGTGGATACAGAGTGGTAAGATTCAGGACAACATACTGTTTGGCAAGCAGATG 2139

Qy        500 GluLysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeu 519
              :::      |||:::|||::::::|||:::::::::|||:::||||||||||||||||||::::::
Db       2140 GATAATGAGAAGTATGACAGGGTCCTCGAGTCATGCTCGCTGAAGAAAGACTTGGAGATA 2199

Qy        520 LeuGluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGln 539
              |||      |||   |||||||||||||||:::|||||||||          ||||||||||||||||||
Db       2200 TTGCCGTTTGGTGACCAGACCGTCATTGGAGAGAGAGGCATCAACCTTAGTGGTGGTCAG 2259

Qy        540 LysAlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAsp 559
              |||   |||:::      :::||||||||:::||||||||||||||||||||||||||||         |||
Db       2260 AAGCAAAGGATTCAGATAGCCCGAGCTCTGTATCAGGATGCAGACATCTATTTGTTTGAT 2319

Qy        560 AspProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCys 579
              ||||||      |||||||||||||||                  |||||||||:::   |||:::
Db       2320 GATCCTTTCAGTGCAGTCGATGCTCATACAGGATCCCACTTGTTCAAGGAATGCTTGCTT 2379

Qy        580 GlnIleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAla 599
                 |||      |||      :::      ||||||||||||:::::::::|||   |||
Db       2380 GGAGAATTGGCTTCAAAAACAGTTGTTTATGTCACTCATCAGATTGAATTCCTACCTGCT 2439

Qy        600 AlaSerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGlu 619
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Db       2440 GCTGATCTTATTCTGGTCATGAAAGGTGGGAGAATAGCACAGGCAGGCAAATATGACGAA 2499

Qy        620 PheLeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGlu 639

Db       2500 ATACTTGGATCAGGGGAAGAGTTCATGGAACTGGTTGGTGCTCACAAGGATGCTCTTACC 2559

Qy        640 GlnProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerVal 659

Db       2560 GCATTGGATGCGATAGATGTCACAAATGGAGGCAACGAGGCTTCCTCTTCTAGTAAGACA 2619

Qy        660 TrpSer---GlnGlnSerSerArgProSerLeuLysAsp-GlyAlaLeuGluSerGlnAs 678

Db       2620 GCAAGCCTGGCCAGGTCAGTGTCAGTTGAGAAGAAAGATAAACAGAATGGAAAAGAAGAC 2679

Qy        678 pThrGluAsnValPro------ValThrLeuSerGluGluAsnArgSerGluGlyLysVa 696

Db       2680 GGATGCCAATGCTCAAAGTGGGCAGCTGGTGCAGGAAGAGGAAAGGGAGAAAGGAAGGGT 2739

Qy        696 lGlyPheGlnAlaTyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePh 716

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Db       2800 CATCTTGCTGGCCCAAATACTTTTCCAAGTACTTCAGATTGCTAGCAATTACTGGATGGC 2859

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Db       2860 C---TGGGCTGCTCCTGTCTCAAAG--------------------------GACGTTGA 2889

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Qy        776 lLeuPheGlyIleAlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnTh 796

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Qy        816 nProIleGlyArgIleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLe 836

Db       3070 TCCTAGTGGGCGCATTTTGAATAGAGCTTCAACGGATCAAAGCGAAGTGGACACCAGCAT 3129

Qy        836 uProLeuThrPheLeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerVa 856

Db       3130 TGCTTACCAGATGGATCTGTTGCATTTTCCATCATACAACTTGTTGGAATTATTGCTGT 3189

Qy        856 lAlaValAlaValIleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIl 876

Db       3190 GATGTCTCAGGTTGCATGGCAGGTTTTTGTTGTTTTTATTCCTGTGCTTGCTGCCTGCTT 3249

Qy        876 ePheLeuArgArgTyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrTh 896

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Qy        956 sAlaMetPheValIleIleValAlaPheGlySerLeuIleLeuAlaLys----------- 972

Db       3490 ATCC---------CTTACATTTGCCTTCTCTTTGATATTTTTGGTCAATCTTCCGACTGG 3540

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Db       3721 GACGCAGGACTGGCCATCAGAAGGAGAAATTATGCTCAATAACGTCCATGTGAGATATGC 3780

Qy       1051 rProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIleLysSerGlnGluLysVa 1071

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Db       4021 CGTGAGAACCAACCTTGATCCTATTGGAGAGTACACTGATAGCCAAATCTGGGAGGCCTT 4080

Qy       1150 uGlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLysMetAspThrGluLe 1170

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Db       4261 CACGGACAACCTCATCCAGAAAACTCTCAGGCAGCAGTTTTCCGACGCGACGGTCATCAC 4320

Qy       1230 rIleAlaHisArgLeuAsnThrIleIleAspSerAspLysIleMetValLeuAspSerGl 1250

Db       4321 AATCGCGCACCGGATCACCTCCGTCCTTGACAGCGACATGGTCTTGCTCCTTGACAACGG 4380

Qy       1250 yArgLeuLysGluTyrAspGluProTyrValLeuLeuGlnAsnLysGluSerLeuPheTy 1270

Db       4381 TGTGGCCGTGGAGCGCGACACGCCGACCAGGCTACTGGAGGACAAGTCGTCTCTCTTCTC 4440

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Db       4441 CAAGCTCGTAGCGGAA 4456
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RESULT 15
CL970490

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LOCUS       CL970490                4425 bp    DNA     linear   GSS 21-SEP-2004
DEFINITION  OsIFCC019970 Oryza sativa Express Library Oryza sativa (indica
            cultivar-group) genomic, genomic survey sequence.
ACCESSION   CL970490
VERSION     CL970490.1  GI:52395588
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KEYWORDS    GSS.
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 4425)
  AUTHORS   Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
            Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
            Wong,G.K.S., Deng,X.W. and Wang,J.
  TITLE     An analysis of transcriptional regulation of the rice genome and
            its comparison to Arabidopsis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Chen Chen
            Department of Bioinformatic
            Beijing Institute of Genomics
            Chinese Academy of Sciences, Beijing 101300, China
            Tel: 86-10-80481559
            Fax: 86-10-80488676
            Email: chenchen@genomics.org.cn
            Rice genomic sequence.
            Class: exon-trapped.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:39946"
                     /clone_lib="Oryza sativa Express Library"
                     /note="Oryza sativa exon trapped genomic sequences "
ORIGIN

Alignment Scores:
Pred. No.:              2.5e-205       Length:          4425
Score:                  1942.50        Matches:         437
Percent Similarity:     53.9%          Conservative:    261
Best Local Similarity:  33.7%          Mismatches:      518
Query Match:            28.6%          Indels:          79
DB:                     10             Gaps:            22

US-09-976-858-42 (1-1325) x CL970490 (1-4425)

Qy         15 AspAlaAsnLeuCysSerArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGly 34
Db        655 GAGGCTGGGTTCCTGAGCAGGTTGCTGTTCACGTGGATGAACCCGTTGCTGCGGCTGGGT 714

Qy         35 HisLysArgArgLeuGluGluAspAspMetTyrSerValLeuProGluAspArgSerGln 54
Db        715 TACTCCAAGCCGCTCGGCCTCGGCGACGTCCCGCCGCTTGACGCCGACGACGAGGCGGCG 774

Qy         55 HisLeuGlyGluGluLeuGlnGlyPheTrpAspLysGluValLeuArg------------ 70
Db        775 CAGGCGTGCGACACGTTCCTGCGAGAATGGCACCGGCGGCGGAGCGCGACGCCGGGCGGC 834

Qy         71 ---AlaGluAsnAspAlaGlnLysProSerLeuThrArgAlaIleIleLysCysTyrTrp 89
Db        835 GGCGGCGAGGAGAAGGCGGCGAGCAGGCTGGTGTTCGCGGTGCTCGCCGCGTGCTACAAG 894

Qy         90 LysSerTyrLeuValLeuGlyIlePheThrLeuIleGluGluSerAlaLysValIleGln 109
Db        895 AAGGACCTCCTCCTGACGGCGCTCTACACGCTGCTCCGGACGGCGGCGTTCGGCGCCATG 954

Qy        110 ProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspProMetAspSerVal 129
Db        955 CCGGTGATGCTCTACTCCCTGGTGTCCTAC------TCCTACCGGCGGCGGGAGCGT--- 1005

Qy        130 AlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThrLeuIleLeuAla 149
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Qy        150 IleLeuHisHisLeuTyrPheTyrHisValGlnCysAlaGlyMetArgLeuArgValAla 169
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Qy        250 LeuGlnSerCys-----------------PheGlyLysLeuPheSerSerLeuArgSer 263
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Db       1408 AGGTTCATGGCGGCGCAGGACGAGCGGCAGCGCGCCACGGCGGAGGCGCTCGGCGCCATG 1467

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Db       1468 AAGGTGGTGAAGCTCCAGTCGTGGGAGGAATTCTTCAGGGGGAACGTGCAGCGGCTGCGC 1527

Qy        304 LysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAlaSer 323
Db       1528 GACGCCGAGGTGCGGTGGCTGGCCGACGCGCAGGTCAGCAAGGCGTACGGCAGCTCGCTA 1587

Qy        324 PhePheSerAlaSerLysIleIleValPheValThrPheThr---ThrTyrValLeuLeu 342
Db       1588 TACTGGATGTCGCCGACCATCATCTCCGCGGTGATCTTCGCCGGCACGGCGGCGCTCCGG 1647

Qy        343 GlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValArg 362
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Qy        383 IleArgArgIleGlnThrPheLeuLeuLeuAspGluIle---------SerGlnArgAsn 399
Db       1765 CTGGACCGCATCGGCAAGTTCCTCATGGAGGAGGAGTTCCGGGACGACGCCGTCCTGCCA 1824

Qy        400 ArgGlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrp 419
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Qy        420 AspLysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGlu 439
Db       1885 GAGCCTAGCAAGGCCATTGCAACACTGAAATCCATCAGCATCGCAGCAATGCAGGGCGAG 1944

Qy        440 LeuLeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeu 459
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Qy        460 GlyGluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSer 479
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Qy        480 GlnGlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyr 499
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Qy        500 GluLysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeu 519
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Db     2185 TTCCCCATGGCGACCTGACGGAGATCGGGCAACGAGGCCTGAACATGAGTGGAGGGCAG 2244

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Db     2425 GTTGACAAGATCCTGGTCATGGAAAATGGGGAGATAACTCAGGAGGGAACTTACAGTGAG 2484

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Db     2485 CTTCTGCAATCCGGCACGGCATTCGAACAGCTTGTG---------AATGCGCACAAGGAC 2535

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Qy      754 AsnValThrGluLysLeuAspLeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrVal 773
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Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
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Db       4300 AGTGACATGGTCATGGTTCTTTCATACGGGAAACTCATAGAGTATGATAGGCCATCAAGG 4359

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGln 1275
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Db       4360 CTGATGGAGAATGAGGACTCTGCCTTCTGTAAGCTTGTAGCTGAG 4404
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Search completed: March 14, 2006, 12:51:30
Job time : 11411 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on:         March 14, 2006, 09:29:33 ; Search time 515 Seconds
                                           (without alignments)
                                           4573.338 Million cell updates/sec

Title:          US-09-976-858-42
Perfect score:  6787
Sequence:       1 MLPVYQEVKPNPLQDANLCS..........MVTNTSNGQPSTLTIFETAL 1325

Scoring table:  BLOSUM62
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                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
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Searched:       1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters:      2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US09976858/runat_13032006_170104_11871/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Database :      Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6779	99.9	4231	3	US-09-647-140B-1	Sequence 1, Appli
2	6760	99.6	6082	3	US-09-439-313-535	Sequence 535, App
3	6760	99.6	6082	3	US-09-636-215-535	Sequence 535, App
4	6760	99.6	6082	3	US-09-685-166A-535	Sequence 535, App
5	6760	99.6	6082	3	US-09-679-426-535	Sequence 535, App
6	6760	99.6	6082	3	US-09-759-143-535	Sequence 535, App
7	6760	99.6	6082	3	US-09-651-236-535	Sequence 535, App
8	6760	99.6	6082	3	US-09-657-279-535	Sequence 535, App
9	6760	99.6	6082	3	US-10-012-896-535	Sequence 535, App
10	6600.5	97.3	6140	3	US-09-439-313-536	Sequence 536, App
11	6600.5	97.3	6140	3	US-09-636-215-536	Sequence 536, App
12	6600.5	97.3	6140	3	US-09-685-166A-536	Sequence 536, App
13	6600.5	97.3	6140	3	US-09-679-426-536	Sequence 536, App
14	6600.5	97.3	6140	3	US-09-759-143-536	Sequence 536, App
15	6600.5	97.3	6140	3	US-09-651-236-536	Sequence 536, App
16	6600.5	97.3	6140	3	US-09-657-279-536	Sequence 536, App
17	6600.5	97.3	6140	3	US-10-012-896-536	Sequence 536, App
18	6357	93.7	4395	3	US-10-012-896-1007	Sequence 1007, Ap
19	6354	93.6	3786	3	US-10-012-896-1006	Sequence 1006, Ap
20	2298.5	33.9	5011	2	US-08-141-893-1	Sequence 1, Appli
21	2298.5	33.9	5011	2	US-08-463-092B-1	Sequence 1, Appli
22	2298.5	33.9	5011	2	US-08-463-092B-3	Sequence 3, Appli
23	2298.5	33.9	5011	2	US-08-462-109A-1	Sequence 1, Appli
24	2298.5	33.9	5011	2	US-08-462-109A-3	Sequence 3, Appli
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32	2263	33.3	5889	2	US-08-463-092B-5	Sequence 5, Appli
33	2263	33.3	5889	2	US-08-462-109A-5	Sequence 5, Appli
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37	2216.5	32.7	5696	3	US-09-976-594-335	Sequence 335, App
38	2145	31.6	5232	3	US-08-972-927-1	Sequence 1, Appli
39	2123	31.3	5079	3	US-09-647-140B-5	Sequence 5, Appli
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43	2087	30.7	6129	2	US-07-637-621-1	Sequence 1, Appli
44	2087	30.7	6129	2	US-08-951-912-1	Sequence 1, Appli
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ALIGNMENTS

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RESULT 1
US-09-647-140B-1
; Sequence 1, Application US/09647140B
; Patent No. 6803184
; GENERAL INFORMATION:
;  APPLICANT: Fox Chase Cancer Center
;  APPLICANT:  Kruh, Gary D.
;  APPLICANT:  Lee, Kun
;  APPLICANT:  Belinsky, Martin G.
;  APPLICANT:  Bain, Lisa J.
;  TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
;  TITLE OF INVENTION:  Nucleic Acids and Methods of Use Thereof
;  FILE REFERENCE: FCCC 98-02
;  CURRENT APPLICATION NUMBER: US/09/647,140B
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: PCT/US99/06644
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,759
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/095,153
;  PRIOR FILING DATE: 1998-08-03
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 4231
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-647-140B-1

Alignment Scores:
Pred. No.:              0              Length:         4231
Score:                  6779.00        Matches:        1323
Percent Similarity:     99.9%          Conservative:   1
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Best Local Similarity:  99.8%        Mismatches:    1
Query Match:            99.9%        Indels:        0
DB:                     3            Gaps:          0

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Db      176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy       41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
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Db      236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy       61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Qy      101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
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Qy      141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
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Qy      181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
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Qy      261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Qy      321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Qy      361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Qy      381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Qy      581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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Qy      621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Qy      661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
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Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Db       2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
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Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Db       2816 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
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Db       2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
              |||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db       3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy       1321 PheGluThrAlaLeu 1325
              |||||||||||||||
Db       4076 TTCGAGACAGCACTG 4090
```

RESULT 2
US-09-439-313-535
; Sequence 535, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

```
;  FILE REFERENCE: 210121.427C9
;  CURRENT APPLICATION NUMBER: US/09/439,313
;  CURRENT FILING DATE:  1999-11-12
;  NUMBER OF SEQ ID NOS: 575
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 535
;   LENGTH: 6082
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-439-313-535

Alignment Scores:
Pred. No.:                 0              Length:        6082
Score:                     6760.00        Matches:       1324
Percent Similarity:        99.9%          Conservative:  0
Best Local Similarity:     99.9%          Mismatches:    1
Query Match:               99.6%          Indels:        1
DB:                        3              Gaps:          0

US-09-976-858-42 (1-1325) x US-09-439-313-535 (1-6082)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 245

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 305

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 365

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 425

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 485

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 545

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 605

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 665

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 725

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 785

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 845

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 905

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 965

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 1025

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1085

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1086 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1145

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1205

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1206 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1265

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1266 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1325

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1385

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1386 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1445

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1446 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1505

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1506 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1565

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1566 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1625

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1626 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1685

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1686 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1745

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1746 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1805

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1806 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1865

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Db       1866 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1925

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1926 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1985

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1986 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 2045

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2046 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2105

Qy          641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2106 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165

Qy          661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2166 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2225

Qy          681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2226 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2285

Qy          701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2286 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2345

Qy          721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2346 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2405

Qy          741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2406 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2465

Qy          761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2525

Qy          781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2526 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2585

Qy          801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2586 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2645

Qy          821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2646 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2705

Qy          841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Db         2706 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2765

Qy          861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2766 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2825

Qy          881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2826 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2885

Qy          901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2886 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2945

Qy          921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2946 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 3005

Qy          941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3006 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 3065

Qy          961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3066 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3125

Qy          981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3126 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3185

Qy         1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3186 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3245

Qy         1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3246 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3305

Qy         1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3306 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3365

Qy         1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3366 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3425

Qy         1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3426 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3485

Qy         1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3486 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3545

Qy         1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3546 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3605

Qy         1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3606 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3665

Qy         1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3666 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3725

Qy         1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3726 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3785

Qy         1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db         3786 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAATC-CGG 3844

Qy         1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3845 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3904

Qy         1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3905 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3964

Qy         1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3965 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 4024

Qy         1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4025 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4084

Qy         1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4085 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4144

Qy         1321 PheGluThrAlaLeu 1325
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Db         4145 TTCGAGACAGCACTG 4159
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RESULT 3
US-09-636-215-535
; Sequence 535, Application US/09636215

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; Patent No. 6620922
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.42717C17
;  CURRENT APPLICATION NUMBER: US/09/636,215
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS:  852
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 535
;   LENGTH: 6082
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-636-215-535

Alignment Scores:
Pred. No.:              0              Length:        6082
Score:                  6760.00        Matches:       1324
Percent Similarity:     99.9%          Conservative:  0
Best Local Similarity:  99.9%          Mismatches:    1
Query Match:            99.6%          Indels:        1
DB:                     3              Gaps:          0

US-09-976-858-42 (1-1325) x US-09-636-215-535 (1-6082)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 245

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 305

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 365

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 425

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 485

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 545

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 605

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 665

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 725

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 785

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 845

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 905

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 965

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 1025

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1085

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1086 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1145

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1205

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1206 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1265

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1266 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1325

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1385

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1386 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1445

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1446 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1505

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1506 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1565

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1566 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1625

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1626 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1685

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1686 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1745
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Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1746 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1805

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1806 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1865

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1866 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1925

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1926 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1985

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1986 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 2045

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2046 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2105

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2106 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2166 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2225

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2226 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2285

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2286 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2345

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2346 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2405

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2406 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2465

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2525

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Db       2526 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2585

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2586 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2645

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Db       2646 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2705

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Db       2706 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2765

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2766 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2825

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2826 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2885

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2886 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2945

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2946 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 3005

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
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Db       3006 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 3065

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3066 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3125

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3126 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3185

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3186 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3245

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3246 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3305

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3306 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3365

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3366 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3425

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3426 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3485

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3486 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3545

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3546 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3605

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3606 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3665

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3666 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3725

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3726 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3785

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       3786 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAATC-CGG 3844

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3845 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3904

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3905 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3964

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3965 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 4024

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4025 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4084

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4085 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4144

Qy       1321 PheGluThrAlaLeu 1325
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Db       4145 TTCGAGACAGCACTG 4159
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RESULT 4
US-09-685-166A-535
; Sequence 535, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-535

Alignment Scores:

Pred. No.:	0	Length:	6082
Score:	6760.00	Matches:	1324
Percent Similarity:	99.9%	Conservative:	0
Best Local Similarity:	99.9%	Mismatches:	1
Query Match:	99.6%	Indels:	1
DB:	3	Gaps:	0

US-09-976-858-42 (1-1325) x US-09-685-166A-535 (1-6082)

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Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 245

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 305

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 365

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 425

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 485

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 545

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 605

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 665

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 725

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 785

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 845

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 905

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 965

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 1025

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1085

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1086 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1145

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1205

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1206 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1265

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1266 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1325

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1385

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1386 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1445
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Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
Db       1446 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1505

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
Db       1506 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1565

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
Db       1566 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1625

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
Db       1626 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1685

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
Db       1686 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1745

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
Db       1746 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1805

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
Db       1806 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1865

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
Db       1866 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1925

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
Db       1926 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1985

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
Db       1986 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 2045

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
Db       2046 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2105

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
Db       2106 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
Db       2166 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2225

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
Db       2226 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2285

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
Db       2286 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2345

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
Db       2346 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2405

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
Db       2406 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2465

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
Db       2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2525

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
Db       2526 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2585

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
Db       2586 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2645

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
Db       2646 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2705

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
Db       2706 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2765

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
Db       2766 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2825

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
Db       2826 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2885

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
Db       2886 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2945

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
Db       2946 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 3005

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
Db       3006 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 3065

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
Db       3066 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3125

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
Db       3126 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3185

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
Db       3186 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3245

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
Db       3246 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3305

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
Db       3306 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3365

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
Db       3366 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3425

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
Db       3426 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3485

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
Db       3486 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3545

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
Db       3546 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3605

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Db       3606 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3665

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
Db       3666 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3725

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
Db       3726 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3785

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
Db       3786 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAATC-CGG 3844

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
Db       3845 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3904

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
Db       3905 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3964

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
Db       3965 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 4024

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
Db       4025 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4084

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
Db       4085 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4144

Qy       1321 PheGluThrAlaLeu 1325
Db       4145 TTCGAGACAGCACTG 4159
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RESULT 5
US-09-679-426-535
; Sequence 535, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-679-426-535

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Alignment Scores:
Pred. No.:                 0           Length:          6082
Score:                     6760.00     Matches:         1324
Percent Similarity:        99.9%       Conservative:    0
Best Local Similarity:     99.9%       Mismatches:      1
Query Match:               99.6%       Indels:          1
DB:                        3           Gaps:            0

US-09-976-858-42 (1-1325) x US-09-679-426-535 (1-6082)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
Db        186 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 245

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
Db        246 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 305

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
Db        306 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 365

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
Db        366 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 425

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
Db        426 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 485

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
Db        486 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 545

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
Db        546 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 605

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
Db        606 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 665

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
Db        666 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 725

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
Db        726 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 785

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
Db        786 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 845

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
Db        846 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 905

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
Db        906 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 965

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
Db        966 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 1025

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
Db       1026 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1085

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
```

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Db       1086 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1145

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
Db       1146 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1205

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
Db       1206 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1265

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
Db       1266 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1325

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
Db       1326 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1385

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
Db       1386 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1445

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
Db       1446 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1505

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
Db       1506 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1565

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
Db       1566 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1625

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
Db       1626 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1685

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
Db       1686 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1745

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
Db       1746 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1805

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
Db       1806 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1865

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
Db       1866 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1925

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
Db       1926 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1985

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
Db       1986 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 2045

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
Db       2046 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2105

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
Db       2106 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
Db       2166 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2225

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
Db       2226 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2285

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
Db       2286 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2345

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
Db       2346 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2405

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
Db       2406 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2465

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
Db       2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2525

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
Db       2526 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2585

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
Db       2586 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2645

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
Db       2646 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2705

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
Db       2706 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2765

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
Db       2766 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2825

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
Db       2826 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2885

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
Db       2886 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2945

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
Db       2946 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 3005

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
Db       3006 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 3065

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
Db       3066 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3125

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
Db       3126 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3185

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
Db       3186 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3245

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
Db       3246 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3305
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Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
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Db       3306 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3365

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3366 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3425

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Db       3426 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3485

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
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Db       3486 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3545

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
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Db       3546 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3605

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3606 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3665

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3666 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3725

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3726 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3785

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
              |||||||||||||||||||||||||||||||||||||||||||||||||||     |||
Db       3786 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAATC-CGG 3844

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3845 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3904

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3905 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3964

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3965 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 4024

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4025 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4084

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
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Db       4085 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4144

Qy       1321 PheGluThrAlaLeu 1325
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Db       4145 TTCGAGACAGCACTG 4159
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RESULT 6
US-09-759-143-535
; Sequence 535, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-535

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Alignment Scores:
Pred. No.:              0            Length:         6082
Score:                  6760.00      Matches:        1324
Percent Similarity:     99.9%        Conservative:   0
Best Local Similarity:  99.9%        Mismatches:     1
Query Match:            99.6%        Indels:         1
DB:                     3            Gaps:           0

US-09-976-858-42 (1-1325) x US-09-759-143-535 (1-6082)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 245

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 305

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 365

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 425

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 485

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 545

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 605

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 665

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 725

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 785

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Db        786 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACGACTG 845

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 905

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 965

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 1025

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Db       1026 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1085

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1086 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1145

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1205

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1206 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1265

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1266 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1325

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1385

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1386 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1445

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1446 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1505

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1506 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1565

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1566 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1625

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1626 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1685

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1686 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1745

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1746 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1805

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1806 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1865

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1866 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1925

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1926 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1985

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1986 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 2045

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Db       2046 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2105

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2106 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2166 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2225

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
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Db       2226 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2285

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Db       2286 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2345

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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Db       2346 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2405

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
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Db       2406 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2465

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2525

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Db       2526 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2585

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Db       2586 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2645

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Db       2646 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2705

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2706 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2765

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2766 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2825

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
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Db       2826 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2885

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Db       2886 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2945

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2946 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 3005
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Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
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Db       3006 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 3065

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3066 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3125

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3126 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3185

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
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Db       3186 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3245

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
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Db       3246 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3305

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3306 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3365

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3366 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3425

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Db       3426 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3485

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3486 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3545

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
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Db       3546 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3605

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Db       3606 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3665

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
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Db       3666 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3725

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3726 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3785

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       3786 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAATC-CGG 3844

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3845 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3904

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3905 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3964

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
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Db       3965 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 4024

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
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Db       4025 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4084

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
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Db       4085 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4144

Qy       1321 PheGluThrAlaLeu 1325
              |||||||||||||||
Db       4145 TTCGAGACAGCACTG 4159
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RESULT 7
US-09-651-236-535
; Sequence 535, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.42718C18
;  CURRENT APPLICATION NUMBER: US/09/651,236
;  CURRENT FILING DATE:  2000-08-29
;  NUMBER OF SEQ ID NOS:  865
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 535
;   LENGTH: 6082
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-651-236-535

Alignment Scores:
Pred. No.:              0            Length:        6082
Score:                  6760.00      Matches:       1324
Percent Similarity:     99.9%        Conservative:  0
Best Local Similarity:  99.9%        Mismatches:    1
Query Match:            99.6%        Indels:        1
DB:                     3            Gaps:          0

US-09-976-858-42 (1-1325) x US-09-651-236-535 (1-6082)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
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Db        186 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 245

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
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Db        246 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 305

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
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Db        306 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 365

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Db        366 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 425

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
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Db        426 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 485
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Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
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Db        486 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 545

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
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Db        546 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 605

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
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Db        606 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 665

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db        666 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 725

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 785

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 845

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Db        846 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 905

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 965

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 1025

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Db       1026 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1085

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Db       1086 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1145

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Db       1146 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1205

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1206 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1265

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1266 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1325

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Db       1326 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1385

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1386 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1445

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1446 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1505

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1506 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1565

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1566 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1625

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1626 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTGGGAAGAAATACGAA 1685

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1686 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1745

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Db       1746 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1805

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1806 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1865

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1866 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1925

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1926 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1985

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1986 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 2045

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Db       2046 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2105

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2106 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
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Db       2166 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2225

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2226 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2285

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2286 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2345

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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Db       2346 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2405

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2406 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2465

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
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Db       2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2525

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Db       2526 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2585

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Db       2586 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2645

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       2646 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2705

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2706 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2765

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2766 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2825

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
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Db       2826 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2885

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Db       2886 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2945

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
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Db       2946 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 3005

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
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Db       3006 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 3065

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3066 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3125

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
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Db       3126 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3185

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
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Db       3186 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3245

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
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Db       3246 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3305

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
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Db       3306 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3365

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
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Db       3366 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3425

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Db       3426 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3485

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
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Db       3486 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3545

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
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Db       3546 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3605

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Db       3606 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3665

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
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Db       3666 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3725

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3726 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3785

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db       3786 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAATC-CGG 3844

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
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Db       3845 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3904

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
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Db       3905 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3964

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
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Db       3965 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 4024

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
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Db       4025 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4084

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
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Db       4085 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4144

Qy       1321 PheGluThrAlaLeu 1325
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Db       4145 TTCGAGACAGCACTG 4159
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RESULT 8
US-09-657-279-535
; Sequence 535, Application US/09657279
; Patent No. 6894146
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C19
;  CURRENT APPLICATION NUMBER: US/09/657,279
;  CURRENT FILING DATE:  2000-09-06
;  NUMBER OF SEQ ID NOS:  877
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 535
;   LENGTH: 6082
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-657-279-535

Alignment Scores:
Pred. No.:               0           Length:        6082
Score:                   6760.00     Matches:       1324
Percent Similarity:      99.9%       Conservative:  0
Best Local Similarity:   99.9%       Mismatches:    1
Query Match:             99.6%       Indels:        1
DB:                      3           Gaps:          0

US-09-976-858-42 (1-1325) x US-09-657-279-535 (1-6082)
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Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
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Db        186 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 245

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
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Db        246 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 305

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 365

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Db        366 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 425

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
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Db        426 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 485

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 545

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 605

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
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Db        606 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 665

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db        666 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 725

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
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Db        726 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 785

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Db        786 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 845

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Db        846 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 905

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 965

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Db        966 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 1025

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Db       1026 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1085

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Db       1086 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1145

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Db       1146 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1205

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Db       1206 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1265

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1266 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1325

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1385

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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Db       1386 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1445

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1446 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1505

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1506 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1565

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1566 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1625

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1626 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1685

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1686 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1745

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Db       1746 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1805

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1806 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1865

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1866 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1925

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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Db       1926 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1985

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1986 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 2045

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Db       2046 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2105

Qy        641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2106 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165

Qy        661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2166 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2225

Qy        681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2226 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2285

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Db       2286 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2345

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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Db         2346 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2405

Qy          741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
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Db         2406 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2465

Qy          761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
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Db         2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2525

Qy          781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Db         2526 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2585

Qy          801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Db         2586 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2645

Qy          821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2646 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2705

Qy          841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2706 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2765

Qy          861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2766 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2825

Qy          881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
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Db         2826 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2885

Qy          901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
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Db         2886 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2945

Qy          921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
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Db         2946 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 3005

Qy          941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3006 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 3065

Qy          961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3066 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3125

Qy          981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3126 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3185

Qy         1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
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Db         3186 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3245

Qy         1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
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Db         3246 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3305

Qy         1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
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Db         3306 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3365

Qy         1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
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Db         3366 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3425

Qy         1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Db         3426 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3485

Qy         1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
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Db         3486 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3545

Qy         1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
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Db         3546 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3605

Qy         1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Db         3606 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3665

Qy         1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
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Db         3666 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3725

Qy         1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3726 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3785

Qy         1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db         3786 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAATC-CGG 3844

Qy         1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3845 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3904

Qy         1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
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Db         3905 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3964

Qy         1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
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Db         3965 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 4024

Qy         1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4025 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4084

Qy         1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
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Db         4085 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4144

Qy         1321 PheGluThrAlaLeu 1325
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Db         4145 TTCGAGACAGCACTG 4159
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RESULT 9
US-10-012-896-535
; Sequence 535, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.

```
; APPLICANT:  Houghton, Raymond L.
; APPLICANT:  Vinals de Bassols, Carlota
; APPLICANT:  Foy, Teresa
; APPLICANT:  Fanger, Gary R.
; APPLICANT:  Wantanabe, Yoshihiro
; APPLICANT:  Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE:  2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 535
;   LENGTH: 6082
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-012-896-535

Alignment Scores:
Pred. No.:              0             Length:        6082
Score:                  6760.00       Matches:       1324
Percent Similarity:     99.9%         Conservative:  0
Best Local Similarity:  99.9%         Mismatches:    1
Query Match:            99.6%         Indels:        1
DB:                     3             Gaps:          0

US-09-976-858-42 (1-1325) x US-10-012-896-535 (1-6082)

Qy      1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
Db    186 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 245

Qy     21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
Db    246 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 305

Qy     41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
Db    306 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 365

Qy     61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
Db    366 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 425

Qy     81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
Db    426 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 485

Qy    101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
Db    486 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 545

Qy    121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
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Qy    141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
Db    606 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 665

Qy    161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
Db    666 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 725

Qy    181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
Db    726 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 785

Qy    201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
Db    786 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 845

Qy    221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
Db    846 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 905

Qy    241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
Db    906 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 965

Qy    261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
Db    966 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 1025

Qy    281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
Db   1026 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1085

Qy    301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
Db   1086 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1145

Qy    321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
Db   1146 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1205

Qy    341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
Db   1206 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1265

Qy    361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
Db   1266 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1325

Qy    381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Qy    401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
Db   1386 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1445

Qy    421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
Db   1446 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1505

Qy    441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
Db   1506 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1565

Qy    461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
Db   1566 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1625

Qy    481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
Db   1626 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1685

Qy    501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
Db   1686 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1745

Qy    521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
Db   1746 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1805

Qy    541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
Db   1806 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1865

Qy    561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
Db   1866 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1925

Qy    581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1926 ATTTTGCATGAGAAGATCACAATTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1985

Qy          601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1986 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 2045

Qy          621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Db         2046 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2105

Qy          641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2106 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165

Qy          661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2166 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2225

Qy          681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2226 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2285

Qy          701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Db         2286 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2345

Qy          721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2346 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2405

Qy          741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2406 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2465

Qy          761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2525

Qy          781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Db         2526 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2585

Qy          801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Db         2586 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2645

Qy          821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2646 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2705

Qy          841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2706 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2765

Qy          861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2766 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2825

Qy          881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2826 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2885

Qy          901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2886 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2945

Qy          921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2946 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 3005

Qy          941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         3006 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 3065

Qy          961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3066 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3125

Qy          981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3126 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3185

Qy         1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3186 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3245

Qy         1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
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Db         3246 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3305

Qy         1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3306 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3365

Qy         1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3366 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3425

Qy         1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Db         3426 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3485

Qy         1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3486 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3545

Qy         1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3546 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3605

Qy         1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3606 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3665

Qy         1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3666 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3725

Qy         1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3726 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3785

Qy         1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
                |||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db         3786 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAATC-CGG 3844

Qy         1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3845 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3904

Qy         1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3905 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3964

Qy         1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3965 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 4024

Qy         1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4025 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4084

Qy         1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4085 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4144
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Qy       1321 PheGluThrAlaLeu 1325
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Db       4145 TTCGAGACAGCACTG 4159

RESULT 10
US-09-439-313-536
; Sequence 536, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan Louise
;  APPLICANT:  Jiang Yuqui
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Kalos, Michael
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Retter, Mark
;  APPLICANT:  Solk, John
;  APPLICANT:  Day, Craig
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C9
;  CURRENT APPLICATION NUMBER: US/09/439,313
;  CURRENT FILING DATE:  1999-11-12
;  NUMBER OF SEQ ID NOS: 575
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 536
;   LENGTH: 6140
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (4535)
;   OTHER INFORMATION: n=A,T,C or G
US-09-439-313-536

Alignment Scores:
Pred. No.:               0              Length:         6140
Score:                   6600.50        Matches:        1300
Percent Similarity:      97.0%          Conservative:   0
Best Local Similarity:   97.0%          Mismatches:     0
Query Match:             97.3%          Indels:         40
DB:                      3              Gaps:           1

US-09-976-858-42 (1-1325) x US-09-439-313-536 (1-6140)

Qy         26 TrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGluGluAspAspMetTyr 45
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Db        235 TGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAGGAAGATGATATGTAT 294

Qy         46 SerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheTrpAsp 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 TCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGGAT 354

Qy         66 LysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArgAlaIleIle 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 AAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCATA 414

Qy         86 LysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGluGluSerAla 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 AAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTAATTGAGGAAAGTGCC 474

Qy        106 LysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspPro 125
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Db        475 AAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTTGAAAATTATGATCCC 534

Qy        126 MetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThr 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 ATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTGCTGACTTTTTGCACG 594

Qy        146 LeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCysAlaGlyMetArg 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 CTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAGTGTGCTGGGATGAGG 654

Qy        166 LeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsnMetAla 185
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Db        655 TTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGTCTTAGTAACATGGCC 714

Qy        186 MetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsnLysPhe 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 ATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAATGATGTGAACAAGTTT 774

Qy        206 AspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIleAlaVal 225
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Db        775 GATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTGCAGGCGATCGCAGTG 834

Qy        226 ThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaValLeuIle 245
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Db        835 ACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGGATGGCAGTTCTAATC 894

Qy        246 IleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLysThr 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 ATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCACTGAGGAGTAAAACT 954

Qy        266 AlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIleArgIle 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGGTATAAGGATA 1014

Qy        286 IleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArgLysLys 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1015 ATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTTGAGAAAGAAG 1074

Qy        306 GluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAlaSerPhePhe 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1075 GAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAATTTGGCTTCGTTTTTC 1134

Qy        326 SerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeuGlySerVal 345
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Db       1135 AGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTGTG 1194

Qy        346 IleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValArgLeuThrVal 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1195 ATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCTGTGCGGCTGACGGTT 1254

Qy        366 ThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIleArgArg 385
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Db       1255 ACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATCGTCAGCATCCGAAGA 1314

Qy        386 IleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuProSerAsp 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1315 ATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGTCAGCTGCCGTCAGAT 1374

Qy        406 GlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThr 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1375 GGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGACC 1434

Qy        426 ProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGly 445
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Db       1435 CCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGCTGTGGTCGGC 1494

Qy        446 ProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSer 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1495 CCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATTGGCCCCAAGT 1554

Qy        466 HisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPhe 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1555 CACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAGCAGCCCTGGGTGTTC 1614

Qy        486 SerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGlu 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1615 TCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAAGGAACGATATGAA 1674

Qy        506 LysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeu 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1675 AAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTG 1734

Qy        526 ThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeu 545
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Db       1735 ACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAAGCACGGGTAAACCTT 1794

Qy        546 AlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaVal 565
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1795 GCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGCAGTA 1854

Qy        566 AspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeuHisGluLys 585
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Db       1855 GATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAATTTTGCATGAGAAG 1914

Qy        586 IleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIle 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1915 ATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATA 1974

Qy        606 LeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIle 625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1975 TTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTATA 2034

Qy        626 AspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProProValProGly 645
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Db       2035 GATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAGGA 2094

Qy        646 ThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGlnGlnSerSer 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2095 ACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCT 2154

Qy        666 ArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnValProValThr 685
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Db       2155 AGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTTACA 2214

Qy        686 LeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLysAsnTyrPhe 705
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Db       2215 CTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAGAATTACTTC 2274

Qy        706 ArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAlaAlaGln 725
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2275 AGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTAAACACTGCAGCTCAG 2334

Qy        726 ValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMetLeu 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2335 GTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAACAAAGTATGCTA 2394

Qy        746 AsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsnTrpTyrLeu 765
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2395 AATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACTGGTACTTA 2454

Qy        766 GlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeu 785
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2455 GGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAGATCTCTATTG 2514

Qy        786 ValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIle 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2515 GTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAAATGTTTGAGTCAATT 2574

Qy        806 LeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArgPhe 825
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2575 CTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGTTTC 2634

Qy        826 SerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGln 845
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2635 TCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGATTTCATCCAG 2694

Qy        846 ThrLeuLeuGlnValValGlyValValSerValAlaValAlaValIleProTrpIleAla 865
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Db       2695 ACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCGCA 2754

Qy        866 IleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGluThr 885
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Db       2755 ATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGATATTTTTTGGAAACG 2814

Qy        886 SerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSerHisLeuSer 905
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Db       2815 TCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGTCA 2874

Qy        906 SerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArgCysGlnGlu 925
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2875 TCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGGTGTCAGGAA 2934

Qy        926 LeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSer 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2935 CTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTTGACAACGTCC 2994

Qy        946 ArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPhe 965
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Db       2995 CGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTCATCATCGTTGCCTTT 3054

Qy        966 GlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyr 985
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Db       3055 GGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGTTTGGCACTGTCCTAT 3114

Qy        986 AlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGluValGluAsn 1005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3115 GCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGTGCTGAAGTTGAGAAT 3174

Qy       1006 MetMetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGluAlaProTrp 1025
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3175 ATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAAAAAGAAGCACCTTGG 3234

Qy       1026 GluTyrGlnLysArgProProProAlaTrpProHisGluGlyValIleIlePheAspAsn 1045
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3235 GAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTGATAATCTTTGACAAT 3294

Qy       1046 ValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIle 1065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3295 GTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCATCTGACAGCACTCATT 3354

Qy       1066 LysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeuIle 1085
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3355 AAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATC 3414

Qy       1086 SerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIleAspLysIleLeuThr 1105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3415 TCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATTGATAAGATCTTGACA 3474

Qy       1106 ThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGluProVal 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3475 ACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTGTT 3534

Qy       1126 LeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThrAspGluGlu 1145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3535 TTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAGCACACGGATGAGGAA 3594

Qy       1146 LeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLys 1165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3595 CTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCTTCCTGGTAAA 3654

Qy       1166 MetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGlnArgGlnLeuVal 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3655 ATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAACTGGTG 3714

Qy       1186 CysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAlaThrAla 1205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3715 TGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATTGATGAAGCGACGGCA 3774

Qy       1206 AsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPheAlaHis 1225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3775 AATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGGGAGAAATTTGCCCAC 3834

Qy       1226 CysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLysIleMet 1245
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Db       3835 TGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGCGACAAGATAATG 3894
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Qy       1246 ValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGlnAsnLys 1265
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Db       3895 GTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTTTTGCTGCAAAATAAA 3954

Qy       1266 GluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGluAlaAlaAlaLeuThr 1285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3955 GAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAAGCCGCTGCCCTCACT 4014

Qy       1286 GluThrAlaLysGln--------------------------------------------- 1290
              |||||||||||||||
Db       4015 GAAACAGCAAAACAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGA 4074

Qy       1290 ------------------------------------------------------------ 1290

Db       4075 CCTCAAGTGATCCACCTGCCTTGGCCTCCCAAACTGCTGAGATTACAGGTGTGAGCCACC 4134

Qy       1291 -------------ValTyrPheLysArgAsnTyrProHisIleGlyHisThrAspHisMe 1306
                           |||||||||||||||||||||||||||||||||||||||||||||||
Db       4135 ACGCCCAGCCTGAGTATACTTCAAAAGAAATTATCCACATATTGGTCACACTGACCACAT 4194

Qy       1306 tValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIlePheGluThrAlaLeu 1325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4195 GGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATTTCGAGACAGCACTG 4252
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RESULT 11
US-09-636-215-536
; Sequence 536, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-636-215-536

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Alignment Scores:
Pred. No.:                 0           Length:          6140
Score:                     6600.50     Matches:         1300
Percent Similarity:        97.0%       Conservative:    0
Best Local Similarity:     97.0%       Mismatches:      0
Query Match:               97.3%       Indels:          40
DB:                        3           Gaps:            1
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US-09-976-858-42 (1-1325) x US-09-636-215-536 (1-6140)

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Qy         26 TrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGluGluAspAspMetTyr 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 TGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAGGAAGATGATATGTAT 294

Qy         46 SerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheTrpAsp 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 TCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGGAT 354

Qy         66 LysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArgAlaIleIle 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 AAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCATA 414

Qy         86 LysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGluGluSerAla 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 AAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTAATTGAGGAAAGTGCC 474

Qy        106 LysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspPro 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 AAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTTGAAAATTATGATCCC 534

Qy        126 MetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThr 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 ATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTGCTGACTTTTTGCACG 594

Qy        146 LeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCysAlaGlyMetArg 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 CTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAGTGTGCTGGGATGAGG 654

Qy        166 LeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsnMetAla 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 TTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGTCTTAGTAACATGGCC 714

Qy        186 MetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsnLysPhe 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 ATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAATGATGTGAACAAGTTT 774

Qy        206 AspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIleAlaVal 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 GATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTGCAGGCGATCGCAGTG 834

Qy        226 ThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaValLeuIle 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 ACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGGATGGCAGTTCTAATC 894

Qy        246 IleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLysThr 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 ATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCACTGAGGAGTAAAACT 954

Qy        266 AlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIleArgIle 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGGTATAAGGATA 1014

Qy        286 IleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArgLysLys 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1015 ATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTTGAGAAAGAAG 1074

Qy        306 GluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAlaSerPhePhe 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1075 GAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAATTTGGCTTCGTTTTTC 1134

Qy        326 SerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeuGlySerVal 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1135 AGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTGTG 1194

Qy        346 IleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValArgLeuThrVal 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1195 ATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCTGTGCGGCTGACGGTT 1254

Qy        366 ThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIleArgArg 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1255 ACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATCGTCAGCATCCGAAGA 1314

Qy        386 IleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuProSerAsp 405
```

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                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1315 ATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGTCAGCTGCCGTCAGAT 1374

Qy          406 GlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThr 425
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1375 GGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGACC 1434

Qy          426 ProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGly 445
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1435 CCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGCTGTGGTCGGC 1494

Qy          446 ProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSer 465
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1495 CCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATTGGCCCCAAGT 1554

Qy          466 HisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPhe 485
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1555 CACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAGCAGCCCTGGGTGTTC 1614

Qy          486 SerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGlu 505
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1615 TCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAAGGAACGATATGAA 1674

Qy          506 LysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeu 525
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1675 AAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTG 1734

Qy          526 ThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeu 545
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Db         1735 ACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAAGCACGGGTAAACCTT 1794

Qy          546 AlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaVal 565
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Db         1795 GCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGCAGTA 1854

Qy          566 AspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeuHisGluLys 585
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1855 GATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAATTTTGCATGAGAAG 1914

Qy          586 IleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIle 605
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1915 ATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATA 1974

Qy          606 LeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIle 625
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1975 TTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTATA 2034

Qy          626 AspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProProValProGly 645
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Db         2035 GATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAGGA 2094

Qy          646 ThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGlnGlnSerSer 665
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Db         2095 ACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCT 2154

Qy          666 ArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnValProValThr 685
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Db         2155 AGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTTACA 2214

Qy          686 LeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLysAsnTyrPhe 705
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2215 CTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAGAATTACTTC 2274

Qy          706 ArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAlaAlaGln 725
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2275 AGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTAAACACTGCAGCTCAG 2334

Qy          726 ValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMetLeu 745
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2335 GTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAACAAAGTATGCTA 2394

Qy          746 AsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsnTrpTyrLeu 765
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Db         2395 AATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACTGGTACTTA 2454

Qy          766 GlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeu 785
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2455 GGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAGATCTCTATTG 2514

Qy          786 ValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIle 805
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2515 GTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAAATGTTTGAGTCAATT 2574

Qy          806 LeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArgPhe 825
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2575 CTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGTTTC 2634

Qy          826 SerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGln 845
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Db         2635 TCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGATTTCATCCAG 2694

Qy          846 ThrLeuLeuGlnValValGlyValValSerValAlaValAlaValIleProTrpIleAla 865
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Db         2695 ACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCGCA 2754

Qy          866 IleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGluThr 885
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2755 ATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGATATTTTTTGGAAACG 2814

Qy          886 SerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSerHisLeuSer 905
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2815 TCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGTCA 2874

Qy          906 SerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArgCysGlnGlu 925
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2875 TCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGGTGTCAGGAA 2934

Qy          926 LeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSer 945
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2935 CTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTTGACAACGTCC 2994

Qy          946 ArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPhe 965
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2995 CGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTCATCATCGTTGCCTTT 3054

Qy          966 GlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyr 985
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3055 GGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGTTTGGCACTGTCCTAT 3114

Qy          986 AlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGluValGluAsn 1005
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3115 GCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGTGCTGAAGTTGAGAAT 3174

Qy         1006 MetMetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGluAlaProTrp 1025
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3175 ATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAAAAAGAAGCACCTTGG 3234

Qy         1026 GluTyrGlnLysArgProProProAlaTrpProHisGluGlyValIleIlePheAspAsn 1045
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3235 GAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTGATAATCTTTGACAAT 3294

Qy         1046 ValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIle 1065
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Db         3295 GTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCATCTGACAGCACTCATT 3354

Qy         1066 LysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeuIle 1085
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3355 AAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATC 3414

Qy         1086 SerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIleAspLysIleLeuThr 1105
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3415 TCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATTGATAAGATCTTGACA 3474

Qy         1106 ThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGluProVal 1125
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3475 ACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTGTT 3534
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Qy       1126 LeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThrAspGluGlu 1145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3535 TTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAGCACACGGATGAGGAA 3594

Qy       1146 LeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLys 1165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3595 CTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCTTCCTGGTAAA 3654

Qy       1166 MetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGlnArgGlnLeuVal 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3655 ATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAACTGGTG 3714

Qy       1186 CysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAlaThrAla 1205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3715 TGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATTGATGAAGCGACGGCA 3774

Qy       1206 AsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPheAlaHis 1225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3775 AATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGGGAGAAATTTGCCCAC 3834

Qy       1226 CysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLysIleMet 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3835 TGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGCGACAAGATAATG 3894

Qy       1246 ValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGlnAsnLys 1265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3895 GTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTTTTGCTGCAAAATAAA 3954

Qy       1266 GluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGluAlaAlaAlaLeuThr 1285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3955 GAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAAGCCGCTGCCCTCACT 4014

Qy       1286 GluThrAlaLysGln--------------------------------------------- 1290
              |||||||||||||||
Db       4015 GAAACAGCAAAACAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGA 4074

Qy       1290 ------------------------------------------------------------ 1290

Db       4075 CCTCAAGTGATCCACCTGCCTTGGCCTCCCAAACTGCTGAGATTACAGGTGTGAGCCACC 4134

Qy       1291 -------------ValTyrPheLysArgAsnTyrProHisIleGlyHisThrAspHisMe 1306
                           |||||||||||||||||||||||||||||||||||||||||||||||
Db       4135 ACGCCCAGCCTGAGTATACTTCAAAAGAAATTATCCACATATTGGTCACACTGACCACAT 4194

Qy       1306 tValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIlePheGluThrAlaLeu 1325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4195 GGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATTTCGAGACAGCACTG 4252
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RESULT 12
US-09-685-166A-536
; Sequence 536, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 536
;   LENGTH: 6140
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(6140)
;   OTHER INFORMATION: n=A,T,C or G
US-09-685-166A-536

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Alignment Scores:
Pred. No.:                 0              Length:          6140
Score:                     6600.50        Matches:         1300
Percent Similarity:        97.0%          Conservative:    0
Best Local Similarity:     97.0%          Mismatches:      0
Query Match:               97.3%          Indels:          40
DB:                        3              Gaps:            1

US-09-976-858-42 (1-1325) x US-09-685-166A-536 (1-6140)

Qy         26 TrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGluGluAspAspMetTyr 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 TGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAGGAAGATGATATGTAT 294

Qy         46 SerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheTrpAsp 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 TCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGGAT 354

Qy         66 LysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArgAlaIleIle 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 AAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCATA 414

Qy         86 LysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGluGluSerAla 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 AAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTAATTGAGGAAAGTGCC 474

Qy        106 LysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspPro 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 AAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTTGAAAATTATGATCCC 534

Qy        126 MetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThr 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 ATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTGCTGACTTTTTGCACG 594

Qy        146 LeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCysAlaGlyMetArg 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 CTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAGTGTGCTGGGATGAGG 654

Qy        166 LeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsnMetAla 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 TTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGTCTTAGTAACATGGCC 714

Qy        186 MetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsnLysPhe 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 ATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAATGATGTGAACAAGTTT 774

Qy        206 AspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIleAlaVal 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 GATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTGCAGGCGATCGCAGTG 834

Qy        226 ThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaValLeuIle 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 ACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGGATGGCAGTTCTAATC 894

Qy        246 IleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLysThr 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 ATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCACTGAGGAGTAAAACT 954
```

```
Qy        266 AlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIleArgIle 285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 GCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGGTATAAGGATA 1014

Qy        286 IleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArgLysLys 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1015 ATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTTGAGAAAGAAG 1074

Qy        306 GluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAlaSerPhePhe 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1075 GAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAATTTGGCTTCGTTTTTC 1134

Qy        326 SerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeuGlySerVal 345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1135 AGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTGTG 1194

Qy        346 IleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValArgLeuThrVal 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1195 ATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCTGTGCGGCTGACGGTT 1254

Qy        366 ThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIleArgArg 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1255 ACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATCGTCAGCATCCGAAGA 1314

Qy        386 IleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuProSerAsp 405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1315 ATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGTCAGCTGCCGTCAGAT 1374

Qy        406 GlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThr 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1375 GGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGACC 1434

Qy        426 ProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGly 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1435 CCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGCTGTGGTCGGC 1494

Qy        446 ProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSer 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1495 CCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATTGGCCCCAAGT 1554

Qy        466 HisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPhe 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1555 CACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAGCAGCCCTGGGTGTTC 1614

Qy        486 SerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGlu 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1615 TCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAAGGAACGATATGAA 1674

Qy        506 LysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeu 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1675 AAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTG 1734

Qy        526 ThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeu 545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1735 ACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAAGCACGGGTAAACCTT 1794

Qy        546 AlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaVal 565
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1795 GCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGCAGTA 1854

Qy        566 AspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeuHisGluLys 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1855 GATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAATTTTGCATGAGAAG 1914

Qy        586 IleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIle 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1915 ATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATA 1974

Qy        606 LeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIle 625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1975 TTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTATA 2034

Qy        626 AspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProProValProGly 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2035 GATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAGGA 2094

Qy        646 ThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGlnGlnSerSer 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2095 ACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCT 2154

Qy        666 ArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnValProValThr 685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2155 AGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTTACA 2214

Qy        686 LeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLysAsnTyrPhe 705
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2215 CTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAGAATTACTTC 2274

Qy        706 ArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAlaAlaGln 725
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2275 AGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTAAACACTGCAGCTCAG 2334

Qy        726 ValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMetLeu 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2335 GTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAACAAAGTATGCTA 2394

Qy        746 AsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsnTrpTyrLeu 765
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2395 AATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACTGGTACTTA 2454

Qy        766 GlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeu 785
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2455 GGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAGATCTCTATTG 2514

Qy        786 ValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIle 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2515 GTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAAATGTTTGAGTCAATT 2574

Qy        806 LeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArgPhe 825
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2575 CTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGTTTC 2634

Qy        826 SerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGln 845
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2635 TCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGATTTCATCCAG 2694

Qy        846 ThrLeuLeuGlnValValGlyValValSerValAlaValAlaValIleProTrpIleAla 865
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2695 ACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCGCA 2754

Qy        866 IleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGluThr 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2755 ATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGATATTTTTTGGAAACG 2814

Qy        886 SerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSerHisLeuSer 905
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2815 TCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGTCA 2874

Qy        906 SerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArgCysGlnGlu 925
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2875 TCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGGTGTCAGGAA 2934

Qy        926 LeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSer 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2935 CTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTTGACAACGTCC 2994

Qy        946 ArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPhe 965
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2995 CGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTCATCATCGTTGCCTTT 3054

Qy        966 GlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyr 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3055 GGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGTTTGGCACTGTCCTAT 3114

Qy        986 AlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGluValGluAsn 1005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       3115 GCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGTGCTGAAGTTGAGAAT 3174

Qy       1006 MetMetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGluAlaProTrp 1025
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3175 ATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAAAAAGAAGCACCTTGG 3234

Qy       1026 GluTyrGlnLysArgProProProAlaTrpProHisGluGlyValIleIlePheAspAsn 1045
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3235 GAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTGATAATCTTTGACAAT 3294

Qy       1046 ValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIle 1065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3295 GTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCATCTGACAGCACTCATT 3354

Qy       1066 LysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeuIle 1085
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3355 AAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATC 3414

Qy       1086 SerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIleAspLysIleLeuThr 1105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3415 TCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATTGATAAGATCTTGACA 3474

Qy       1106 ThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGluProVal 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3475 ACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTGTT 3534

Qy       1126 LeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThrAspGluGlu 1145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3535 TTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAGCACACGGATGAGGAA 3594

Qy       1146 LeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLys 1165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3595 CTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCTTCCTGGTAAA 3654

Qy       1166 MetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGlnArgGlnLeuVal 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3655 ATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAACTGGTG 3714

Qy       1186 CysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAlaThrAla 1205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3715 TGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATTGATGAAGCGACGGCA 3774

Qy       1206 AsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPheAlaHis 1225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3775 AATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGGGAGAAATTTGCCCAC 3834

Qy       1226 CysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLysIleMet 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3835 TGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGCGACAAGATAATG 3894

Qy       1246 ValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGlnAsnLys 1265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3895 GTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTTTTGCTGCAAAATAAA 3954

Qy       1266 GluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGluAlaAlaAlaLeuThr 1285
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Db       3955 GAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAAGCCGCTGCCCTCACT 4014

Qy       1286 GluThrAlaLysGln--------------------------------------------- 1290
              |||||||||||||||
Db       4015 GAAACAGCAAAACAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGA 4074

Qy       1290 ------------------------------------------------------------ 1290

Db       4075 CCTCAAGTGATCCACCTGCCTTGGCCTCCCAAACTGCTGAGATTACAGGTGTGAGCCACC 4134

Qy       1291 -------------ValTyrPheLysArgAsnTyrProHisIleGlyHisThrAspHisMe 1306
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Db       4135 ACGCCCAGCCTGAGTATACTTCAAAAGAAATTATCCACATATTGGTCACACTGACCACAT 4194

Qy       1306 tValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIlePheGluThrAlaLeu 1325
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Db       4195 GGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATTTTCGAGACAGCACTG 4252
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RESULT 13
US-09-679-426-536
; Sequence 536, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C20
;  CURRENT APPLICATION NUMBER: US/09/679,426
;  CURRENT FILING DATE:  2000-10-02
;  NUMBER OF SEQ ID NOS:  895
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 536
;   LENGTH: 6140
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(6140)
;   OTHER INFORMATION: n=A,T,C or G
US-09-679-426-536

Alignment Scores:
Pred. No.:                0              Length:         6140
Score:                    6600.50        Matches:        1300
Percent Similarity:       97.0%          Conservative:   0
Best Local Similarity:    97.0%          Mismatches:     0
Query Match:              97.3%          Indels:         40
DB:                       3              Gaps:           1

US-09-976-858-42 (1-1325) x US-09-679-426-536 (1-6140)

Qy         26 TrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGluGluAspAspMetTyr 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 TGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAGGAAGATGATATGTAT 294

Qy         46 SerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheTrpAsp 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 TCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGGAT 354

Qy         66 LysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArgAlaIleIle 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 AAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCATA 414

Qy         86 LysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGluGluSerAla 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 AAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTAATTGAGGAAAGTGCC 474

Qy        106 LysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspPro 125
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Db        475 AAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTTGAAAATTATGATCCC 534

Qy        126 MetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThr 145
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Db        535 ATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTGCTGACTTTTTGCACG 594
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Qy    146 LeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCysAlaGlyMetArg 165
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Db    595 CTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAGTGTGCTGGGATGAGG 654

Qy    166 LeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsnMetAla 185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    655 TTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGTCTTAGTAACATGGCC 714

Qy    186 MetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsnLysPhe 205
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Db    715 ATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAATGATGTGAACAAGTTT 774

Qy    206 AspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIleAlaVal 225
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    775 GATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTGCAGGCGATCGCAGTG 834

Qy    226 ThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaValLeuIle 245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    835 ACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGGATGGCAGTTCTAATC 894

Qy    246 IleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLysThr 265
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Db    895 ATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCACTGAGGAGTAAAACT 954

Qy    266 AlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIleArgIle 285
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    955 GCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGGTATAAGGATA 1014

Qy    286 IleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArgLysLys 305
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Db   1015 ATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTTGAGAAAGAAG 1074

Qy    306 GluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAlaSerPhePhe 325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1075 GAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAATTTGGCTTCGTTTTTC 1134

Qy    326 SerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeuGlySerVal 345
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Db   1135 AGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTGTG 1194

Qy    346 IleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValArgLeuThrVal 365
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Db   1195 ATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCTGTGCGGCTGACGGTT 1254

Qy    366 ThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIleArgArg 385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1255 ACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATCGTCAGCATCCGAAGA 1314

Qy    386 IleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuProSerAsp 405
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Db   1315 ATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGTCAGCTGCCGTCAGAT 1374

Qy    406 GlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThr 425
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Db   1375 GGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGACC 1434

Qy    426 ProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGly 445
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Db   1435 CCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGCTGTGGTCGGC 1494

Qy    446 ProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSer 465
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Db   1495 CCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATTGGCCCCAAGT 1554

Qy    466 HisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPhe 485
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1555 CACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAGCAGCCCTGGGTGTTC 1614

Qy    486 SerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGlu 505
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Db   1615 TCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAAGGAACGATATGAA 1674

Qy    506 LysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeu 525
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Db   1675 AAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTG 1734

Qy    526 ThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeu 545
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Db   1735 ACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAAGCACGGGTAAACCTT 1794

Qy    546 AlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaVal 565
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Db   1795 GCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGCAGTA 1854

Qy    566 AspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeuHisGluLys 585
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Db   1855 GATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAATTTTGCATGAGAAG 1914

Qy    586 IleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIle 605
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Db   1915 ATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATA 1974

Qy    606 LeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIle 625
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Db   1975 TTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTATA 2034

Qy    626 AspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProProValProGly 645
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Db   2035 GATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAGGA 2094

Qy    646 ThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGlnGlnSerSer 665
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Db   2095 ACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCT 2154

Qy    666 ArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnValProValThr 685
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Db   2155 AGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTTACA 2214

Qy    686 LeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLysAsnTyrPhe 705
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Db   2215 CTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAGAATTACTTC 2274

Qy    706 ArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAlaAlaGln 725
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Db   2275 AGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTAAACACTGCAGCTCAG 2334

Qy    726 ValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMetLeu 745
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Db   2335 GTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAACAAAGTATGCTA 2394

Qy    746 AsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsnTrpTyrLeu 765
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Db   2395 AATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACTGGTACTTA 2454

Qy    766 GlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeu 785
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Db   2455 GGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAGATCTCTATTG 2514

Qy    786 ValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIle 805
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Db   2515 GTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAAATGTTTGAGTCAATT 2574

Qy    806 LeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArgPhe 825
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Db   2575 CTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGTTTC 2634

Qy    826 SerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGln 845
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Qy    866 IleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGluThr 885
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Db          2755 ATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGATATTTTTTGGAAACG 2814

Qy           886 SerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSerHisLeuSer 905
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2815 TCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGTCA 2874

Qy           906 SerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArgCysGlnGlu 925
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Db          2875 TCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGGTGTCAGGAA 2934

Qy           926 LeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSer 945
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Db          2935 CTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTTGACAACGTCC 2994

Qy           946 ArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPhe 965
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Qy           986 AlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGluValGluAsn 1005
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Qy          1006 MetMetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGluAlaProTrp 1025
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Db          3175 ATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAAAAAGAAGCACCTTGG 3234

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Qy          1046 ValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIle 1065
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Qy          1066 LysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeuIle 1085
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Db          3355 AAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATC 3414

Qy          1086 SerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIleAspLysIleLeuThr 1105
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Db          3415 TCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATTGATAAGATCTTGACA 3474

Qy          1106 ThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGluProVal 1125
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Db          3475 ACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTGTT 3534

Qy          1126 LeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThrAspGluGlu 1145
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Qy          1146 LeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLys 1165
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Db          3835 TGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGCGACAAGATAATG 3894

Qy          1246 ValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGlnAsnLys 1265
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Qy          1266 GluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGluAlaAlaAlaLeuThr 1285
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Db          3955 GAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAAGCCGCTGCCCTCACT 4014

Qy          1286 GluThrAlaLysGln--------------------------------------------- 1290
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Db          4015 GAAACAGCAAAACAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGA 4074

Qy          1290 ------------------------------------------------------------ 1290

Db          4075 CCTCAAGTGATCCACCTGCCTTGGCCTCCCAAACTGCTGAGATTACAGGTGTGAGCCACC 4134

Qy          1291 -------------ValTyrPheLysArgAsnTyrProHisIleGlyHisThrAspHisMe 1306
                              |||||||||||||||||||||||||||||||||||||||||||||||
Db          4135 ACGCCCAGCCTGAGTATACTTCAAAAGAAATTATCCACATATTGGTCACACTGACCACAT 4194

Qy          1306 tValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIlePheGluThrAlaLeu 1325
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4195 GGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATTTTCGAGACAGCACTG 4252
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RESULT 14
US-09-759-143-536
; Sequence 536, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-759-143-536

Alignment Scores:

Pred. No.:	0	Length:	6140
Score:	6600.50	Matches:	1300
Percent Similarity:	97.0%	Conservative:	0
Best Local Similarity:	97.0%	Mismatches:	0
Query Match:	97.3%	Indels:	40
DB:	3	Gaps:	1

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US-09-976-858-42 (1-1325) x US-09-759-143-536 (1-6140)

Qy       26 TrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGluGluAspAspMetTyr 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      235 TGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAGGAAGATGATATGTAT 294

Qy       46 SerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheTrpAsp 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      295 TCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGGAT 354

Qy       66 LysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArgAlaIleIle 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      355 AAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCATA 414

Qy       86 LysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGluGluSerAla 105
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      415 AAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTAATTGAGGAAAGTGCC 474

Qy      106 LysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspPro 125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      475 AAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTTGAAAATTATGATCCC 534

Qy      126 MetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThr 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      535 ATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTGCTGACTTTTTGCACG 594

Qy      146 LeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCysAlaGlyMetArg 165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      595 CTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAGTGTGCTGGGATGAGG 654

Qy      166 LeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsnMetAla 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      655 TTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGTCTTAGTAACATGGCC 714

Qy      186 MetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsnLysPhe 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      715 ATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAATGATGTGAACAAGTTT 774

Qy      206 AspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIleAlaVal 225
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      775 GATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTGCAGGCGATCGCAGTG 834

Qy      226 ThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaValLeuIle 245
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      835 ACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGGATGGCAGTTCTAATC 894

Qy      246 IleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLysThr 265
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      895 ATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCACTGAGGAGTAAAACT 954

Qy      266 AlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIleArgIle 285
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      955 GCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGGTATAAGGATA 1014

Qy      286 IleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArgLysLys 305
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1015 ATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTTGAGAAAGAAG 1074

Qy      306 GluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAlaSerPhePhe 325
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1075 GAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAATTTGGCTTCGTTTTTC 1134

Qy      326 SerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeuGlySerVal 345
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1135 AGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTGTG 1194

Qy      346 IleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValArgLeuThrVal 365
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1195 ATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCTGTGCGGCTGACGGTT 1254

Qy      366 ThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIleArgArg 385
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1255 ACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATCGTCAGCATCCGAAGA 1314

Qy      386 IleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuProSerAsp 405
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1315 ATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGTCAGCTGCCGTCAGAT 1374

Qy      406 GlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThr 425
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1375 GGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGACC 1434

Qy      426 ProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGly 445
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1435 CCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGCTGTGGTCGGC 1494

Qy      446 ProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSer 465
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1495 CCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATTGGCCCCAAGT 1554

Qy      466 HisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPhe 485
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1555 CACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAGCAGCCCTGGGTGTTC 1614

Qy      486 SerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGlu 505
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1615 TCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAAGGAACGATATGAA 1674

Qy      506 LysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeu 525
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1675 AAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTG 1734

Qy      526 ThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeu 545
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Db     1735 ACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAAGCACGGGTAAACCTT 1794

Qy      546 AlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaVal 565
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1795 GCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGCAGTA 1854

Qy      566 AspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeuHisGluLys 585
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1855 GATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAATTTTGCATGAGAAG 1914

Qy      586 IleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIle 605
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1915 ATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATA 1974

Qy      606 LeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIle 625
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1975 TTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTATA 2034

Qy      626 AspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProProValProGly 645
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Db     2035 GATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAGGA 2094

Qy      646 ThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGlnGlnSerSer 665
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Db     2095 ACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCT 2154

Qy      666 ArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnValProValThr 685
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2155 AGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTTACA 2214

Qy      686 LeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLysAsnTyrPhe 705
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2215 CTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAGAATTACTTC 2274

Qy      706 ArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAlaAlaGln 725
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Db     2275 AGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTAAACACTGCAGCTCAG 2334

Qy      726 ValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMetLeu 745
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2335 GTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAACAAAGTATGCTA 2394
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Qy        746 AsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsnTrpTyrLeu 765
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2395 AATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACTGGTACTTA 2454

Qy        766 GlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeu 785
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2455 GGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAGATCTCTATTG 2514

Qy        786 ValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIle 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2515 GTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAAATGTTTGAGTCAATT 2574

Qy        806 LeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArgPhe 825
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2575 CTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGTTTC 2634

Qy        826 SerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGln 845
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Db       2635 TCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTAGATTTCATCCAG 2694

Qy        846 ThrLeuLeuGlnValValGlyValValSerValAlaValAlaValIleProTrpIleAla 865
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Db       2695 ACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCGCA 2754

Qy        866 IleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGluThr 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2755 ATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGATATTTTTTGGAAACG 2814

Qy        886 SerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSerHisLeuSer 905
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2815 TCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGTCA 2874

Qy        906 SerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArgCysGlnGlu 925
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2875 TCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGGTGTCAGGAA 2934

Qy        926 LeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSer 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2935 CTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTTGACAACGTCC 2994

Qy        946 ArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPhe 965
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2995 CGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTCATCATCGTTGCCTTT 3054

Qy        966 GlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyr 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3055 GGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGTTTGGCACTGTCCTAT 3114

Qy        986 AlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGluValGluAsn 1005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3115 GCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGTGCTGAAGTTGAGAAT 3174

Qy       1006 MetMetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGluAlaProTrp 1025
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3175 ATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAAAAAGAAGCACCTTGG 3234

Qy       1026 GluTyrGlnLysArgProProProAlaTrpProHisGluGlyValIleIlePheAspAsn 1045
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Db       3235 GAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTGATAATCTTTGACAAT 3294

Qy       1046 ValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIle 1065
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Db       3295 GTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCATCTGACAGCACTCATT 3354

Qy       1066 LysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeuIle 1085
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3355 AAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATC 3414

Qy       1086 SerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIleAspLysIleLeuThr 1105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3415 TCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATTGATAAGATCTTGACA 3474

Qy       1106 ThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGluProVal 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3475 ACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTGTT 3534

Qy       1126 LeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThrAspGluGlu 1145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3535 TTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAGCACACGGATGAGGAA 3594

Qy       1146 LeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLys 1165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3595 CTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCTTCCTGGTAAA 3654

Qy       1166 MetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGlnArgGlnLeuVal 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3655 ATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAACTGGTG 3714

Qy       1186 CysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAlaThrAla 1205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3715 TGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATTGATGAAGCGACGGCA 3774

Qy       1206 AsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPheAlaHis 1225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3775 AATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGGGAGAAATTTGCCCAC 3834

Qy       1226 CysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLysIleMet 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3835 TGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGCGACAAGATAATG 3894

Qy       1246 ValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGlnAsnLys 1265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3895 GTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTTTTGCTGCAAAATAAA 3954

Qy       1266 GluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGluAlaAlaLeuThr 1285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3955 GAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAAGCCGCTGCCCTCACT 4014

Qy       1286 GluThrAlaLysGln--------------------------------------------- 1290
              |||||||||||||||
Db       4015 GAAACAGCAAAACAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGA 4074

Qy       1290 ------------------------------------------------------------ 1290

Db       4075 CCTCAAGTGATCCACCTGCCTTGGCCTCCCAAACTGCTGAGATTACAGGTGTGAGCCACC 4134

Qy       1291 -------------ValTyrPheLysArgAsnTyrProHisIleGlyHisThrAspHisMe 1306
                           |||||||||||||||||||||||||||||||||||||||||||||||
Db       4135 ACGCCCAGCCTGAGTATACTTCAAAAGAAATTATCCACATATTGGTCACACTGACCACAT 4194

Qy       1306 tValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIlePheGluThrAlaLeu 1325
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Db       4195 GGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATTTTCGAGACAGCACTG 4252
```

RESULT 15
US-09-651-236-536
; Sequence 536, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William

```
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.42718C18
;  CURRENT APPLICATION NUMBER: US/09/651,236
;  CURRENT FILING DATE:  2000-08-29
;  NUMBER OF SEQ ID NOS:  865
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 536
;   LENGTH: 6140
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(6140)
;   OTHER INFORMATION: n=A,T,C or G
US-09-651-236-536

Alignment Scores:
Pred. No.:              0              Length:         6140
Score:                  6600.50        Matches:        1300
Percent Similarity:     97.0%          Conservative:   0
Best Local Similarity:  97.0%          Mismatches:     0
Query Match:            97.3%          Indels:         40
DB:                     3              Gaps:           1

US-09-976-858-42 (1-1325) x US-09-651-236-536 (1-6140)

Qy         26 TrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGluGluAspAspMetTyr 45
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Db        235 TGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAGGAAGATGATATGTAT 294

Qy         46 SerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheTrpAsp 65
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Db        295 TCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGGAT 354

Qy         66 LysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArgAlaIleIle 85
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Db        355 AAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCATA 414

Qy         86 LysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGluGluSerAla 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 AAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTAATTGAGGAAAGTGCC 474

Qy        106 LysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspPro 125
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Db        475 AAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTTGAAAATTATGATCCC 534

Qy        126 MetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThr 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 ATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTGCTGACTTTTTGCACG 594

Qy        146 LeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCysAlaGlyMetArg 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 CTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAGTGTGCTGGGATGAGG 654

Qy        166 LeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsnMetAla 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 TTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGTCTTAGTAACATGGCC 714

Qy        186 MetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsnLysPhe 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 ATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAATGATGTGAACAAGTTT 774

Qy        206 AspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIleAlaVal 225
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Db        775 GATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTGCAGGCGATCGCAGTG 834

Qy        226 ThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaValLeuIle 245
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Db        835 ACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGGATGGCAGTTCTAATC 894

Qy        246 IleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLysThr 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        895 ATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCACTGAGGAGTAAAACT 954

Qy        266 AlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIleArgIle 285
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Db        955 GCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGGTATAAGGATA 1014

Qy        286 IleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArgLysLys 305
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Db       1015 ATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTTGAGAAAGAAG 1074

Qy        306 GluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAlaSerPhePhe 325
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Db       1075 GAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAATTTGGCTTCGTTTTTC 1134

Qy        326 SerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeuGlySerVal 345
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Db       1135 AGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTGTG 1194

Qy        346 IleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValArgLeuThrVal 365
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Db       1195 ATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCTGTGCGGCTGACGGTT 1254

Qy        366 ThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIleArgArg 385
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Db       1255 ACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATCGTCAGCATCCGAAGA 1314

Qy        386 IleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuProSerAsp 405
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Db       1315 ATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGTCAGCTGCCGTCAGAT 1374

Qy        406 GlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThr 425
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Db       1375 GGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGACC 1434

Qy        426 ProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGly 445
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Db       1435 CCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGCTGTGGTCGGC 1494

Qy        446 ProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSer 465
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Db       1495 CCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATTGGCCCCAAGT 1554

Qy        466 HisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPhe 485
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Db       1555 CACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAGCAGCCCTGGGTGTTC 1614

Qy        486 SerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGlu 505
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Db       1615 TCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAAGGAACGATATGAA 1674

Qy        506 LysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeu 525
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Db       1675 AAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTG 1734

Qy        526 ThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeu 545
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Db       1735 ACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAAGCACGGGTAAACCTT 1794

Qy        546 AlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaVal 565
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Db       1795 GCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGCAGTA 1854

Qy        566 AspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeuHisGluLys 585
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Db       1855 GATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAATTTTGCATGAGAAG 1914

Qy        586 IleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIle 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1915 ATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATA 1974

Qy        606 LeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIle 625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1975 TTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTATA 2034
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Qy        626 AspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProProValProGly 645
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Db       2035 GATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAGGA 2094

Qy        646 ThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGlnGlnSerSer 665
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Db       2095 ACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCT 2154

Qy        666 ArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnValProValThr 685
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Db       2155 AGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTTACA 2214

Qy        686 LeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLysAsnTyrPhe 705
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Db       2215 CTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAGAATTACTTC 2274

Qy        706 ArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAlaAlaGln 725
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Db       2275 AGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTAAACACTGCAGCTCAG 2334

Qy        726 ValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMetLeu 745
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Db       2335 GTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAACAAAGTATGCTA 2394

Qy        746 AsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsnTrpTyrLeu 765
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Db       2395 AATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACTGGTACTTA 2454

Qy        766 GlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeu 785
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Db       2455 GGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAGATCTCTATTG 2514

Qy        786 ValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIle 805
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Db       2515 GTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAAATGTTTGAGTCAATT 2574

Qy        806 LeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArgPhe 825
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Db       2575 CTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGTTTC 2634

Qy        826 SerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGln 845
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Db       2635 TCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGATTTCATCCAG 2694

Qy        846 ThrLeuLeuGlnValValGlyValValSerValAlaValAlaValIleProTrpIleAla 865
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Db       2695 ACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCGCA 2754

Qy        866 IleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGluThr 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2755 ATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGATATTTTTTGGAAACG 2814

Qy        886 SerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSerHisLeuSer 905
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Db       2815 TCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGTCA 2874

Qy        906 SerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArgCysGlnGlu 925
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Db       2875 TCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGGTGTCAGGAA 2934

Qy        926 LeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSer 945
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Db       2935 CTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTTGACAACGTCC 2994

Qy        946 ArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPhe 965
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Db       2995 CGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTCATCATCGTTGCCTTT 3054

Qy        966 GlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyr 985
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Db       3055 GGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGTTTGGCACTGTCCTAT 3114

Qy        986 AlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGluValGluAsn 1005
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Db       3115 GCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGTGCTGAAGTTGAGAAT 3174

Qy       1006 MetMetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGluAlaProTrp 1025
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Db       3175 ATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAAAAAGAAGCACCTTGG 3234

Qy       1026 GluTyrGlnLysArgProProProAlaTrpProHisGluGlyValIleIlePheAspAsn 1045
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Db       3235 GAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTGATAATCTTTGACAAT 3294

Qy       1046 ValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIle 1065
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Db       3295 GTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCATCTGACAGCACTCATT 3354

Qy       1066 LysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeuIle 1085
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Db       3355 AAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATC 3414

Qy       1086 SerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIleAspLysIleLeuThr 1105
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Db       3415 TCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATTGATAAGATCTTGACA 3474

Qy       1106 ThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGluProVal 1125
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Db       3475 ACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTGTT 3534

Qy       1126 LeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThrAspGluGlu 1145
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Db       3535 TTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAGCACACGGATGAGGAA 3594

Qy       1146 LeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLys 1165
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Qy       1166 MetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGlnArgGlnLeuVal 1185
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Db       3655 ATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAACTGGTG 3714

Qy       1186 CysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAlaThrAla 1205
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Db       3715 TGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATTGATGAAGCGACGGCA 3774

Qy       1206 AsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPheAlaHis 1225
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Db       3775 AATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGGGAGAAATTTGCCCAC 3834

Qy       1226 CysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLysIleMet 1245
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Db       3835 TGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGCGACAAGATAATG 3894

Qy       1246 ValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGlnAsnLys 1265
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Qy       1266 GluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGluAlaAlaAlaLeuThr 1285
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Db       3955 GAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAAGCCGCTGCCCTCACT 4014

Qy       1286 GluThrAlaLysGln--------------------------------------------- 1290
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Db       4015 GAAACAGCAAAACAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGA 4074

Qy       1290 ------------------------------------------------------------ 1290

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Qy       1291 -------------ValTyrPheLysArgAsnTyrProHisIleGlyHisThrAspHisMe 1306
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Db       4135 ACGCCCAGCCTGAGTATACTTCAAAAGAAATTATCCACATATTGGTCACACTGACCACAT 4194

Qy       1306 tValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIlePheGluThrAlaLeu 1325
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Db       4195 GGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATTTTCGAGACAGCACTG 4252

Search completed: March 14, 2006, 13:53:46
Job time : 763 secs
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OM protein - nucleic search, using frame_plus_p2n model

Run on:         March 14, 2006, 15:52:06 ; Search time 1653 Seconds
                                           (without alignments)
                                           1849.467 Million cell updates/sec

Title:          US-09-976-858-42
Perfect score:  6787
Sequence:       1 MLPVYQEVKPNPLQDANLCS..........MVTNTSNGQPSTLTIFETAL 1325

Scoring table:  BLOSUM62
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                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       7673375 seqs, 1153648444 residues

Total number of hits satisfying chosen parameters:      15346750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US09976858/runat_13032006_170113_12084/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02h
-USER=US09976858_@CGN_1_1_431_@runat_13032006_170113_12084 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      Published_Applications_NA_New:*
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                13:  /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

  Pred. No. is the number of results predicted by chance to have a
  score greater than or equal to the score of the result being printed,
  and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6787	100.0	5716	12	US-11-124-367A-149	Sequence 149, App
2	6779	99.9	4231	7	US-10-329-258-9	Sequence 9, Appli
3	6760	99.6	6082	12	US-11-234-786-535	Sequence 535, App
4	6686	98.5	5875	12	US-11-091-883-414	Sequence 414, App
5	6600.5	97.3	6140	12	US-11-234-786-536	Sequence 536, App
6	3310.5	48.8	2143	12	US-11-124-367A-150	Sequence 150, App
7	3262	48.1	2256	12	US-11-124-367A-148	Sequence 148, App
8	2285.5	33.7	5011	7	US-10-826-585-35	Sequence 35, Appl
9	2285.5	33.7	5011	12	US-11-045-578-3	Sequence 3, Appli
10	2263	33.3	4587	12	US-11-045-578-2	Sequence 2, Appli
11	2235	32.9	4599	12	US-11-045-578-1	Sequence 1, Appli
12	2227	32.8	4551	7	US-10-932-182A-484	Sequence 484, App
13	2227	32.8	4551	7	US-10-932-182A-484	Sequence 484, App
14	2201	32.4	4954	12	US-11-136-527-2145	Sequence 2145, Ap
15	2174	32.0	5189	12	US-11-136-527-475	Sequence 475, App
16	2087	30.7	6129	7	US-10-501-035-124	Sequence 124, App
17	2087	30.7	6129	9	US-11-206-139-1	Sequence 1, Appli
18	2087	30.7	6129	12	US-11-127-832-24	Sequence 24, Appl
19	2052	30.2	5762	12	US-11-136-527-489	Sequence 489, App
20	2037.5	30.0	5139	12	US-11-132-864-47	Sequence 47, Appl
21	2037.5	30.0	5143	12	US-11-054-168B-20	Sequence 20, Appl
22	1988	29.3	3918	9	US-11-096-568A-29801	Sequence 29801, A
23	1887.5	27.8	4434	7	US-10-932-182A-76875	Sequence 76875, A
24	1887.5	27.8	4434	7	US-10-932-182A-76875	Sequence 76875, A
25	1867	27.5	4986	7	US-10-932-182A-1658	Sequence 1658, Ap
26	1867	27.5	4986	7	US-10-932-182A-1658	Sequence 1658, Ap
27	1843.5	27.2	4686	7	US-10-932-182A-3096	Sequence 3096, Ap
28	1843.5	27.2	4686	7	US-10-932-182A-3096	Sequence 3096, Ap
29	1825	26.9	4680	7	US-10-932-182A-191051	Sequence 191051,
30	1825	26.9	4680	7	US-10-932-182A-191051	Sequence 191051,
31	1802.5	26.6	5792	12	US-11-136-527-2846	Sequence 2846, Ap
32	1760	25.9	4826	12	US-11-090-439-23	Sequence 23, Appl
33	1748	25.8	4977	12	US-11-090-439-25	Sequence 25, Appl
34	1661	24.5	3357	7	US-10-932-182A-80104	Sequence 80104, A
35	1661	24.5	3357	7	US-10-932-182A-80104	Sequence 80104, A
36	1650.5	24.3	4999	8	US-10-995-561-10	Sequence 10, Appl
37	1649	24.3	5064	8	US-10-995-561-9	Sequence 9, Appli
38	1557.5	22.9	3910	8	US-10-995-561-451	Sequence 451, App
39	1543.5	22.7	2682	7	US-10-932-182A-5556	Sequence 5556, Ap
40	1543.5	22.7	2682	7	US-10-932-182A-5556	Sequence 5556, Ap
41	1537.5	22.7	3001	12	US-11-136-527-1015	Sequence 1015, Ap
42	1408	20.7	4863	12	US-11-128-061-958	Sequence 958, App
43	1408	20.7	4863	12	US-11-128-049-958	Sequence 958, App
44	1241.5	18.3	3243	7	US-10-932-182A-81883	Sequence 81883, A
45	1241.5	18.3	3243	7	US-10-932-182A-81883	Sequence 81883, A

ALIGNMENTS

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RESULT 1
US-11-124-367A-149
; Sequence 149, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
;  APPLICANT: Michele Cargill
;  APPLICANT:  Hongjin Huang
;  TITLE OF INVENTION: Genetic Polymorphisms Associated with
;  TITLE OF INVENTION:  Fibrosis Methods of Detection and Uses Thereof
;  FILE REFERENCE: CL001519.ORD
;  CURRENT APPLICATION NUMBER: US/11/124,367A
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US 60/568,846
;  PRIOR FILING DATE: 2004-05-07
;  PRIOR APPLICATION NUMBER: US 60/582,609
;  PRIOR FILING DATE: 2004-06-25
;  PRIOR APPLICATION NUMBER: US 60/599,554
;  PRIOR FILING DATE: 2004-08-09
;  NUMBER OF SEQ ID NOS: 34460
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
;   LENGTH: 5716
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-124-367A-149

Alignment Scores:
Pred. No.:               0              Length:        5716
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Score:                    6787.00    Matches:          1325
Percent Similarity:       100.0%     Conservative:     0
Best Local Similarity:    100.0%     Mismatches:       0
Query Match:              100.0%     Indels:           0
DB:                       12         Gaps:             0

US-09-976-858-42 (1-1325) x US-11-124-367A-149 (1-5716)

Qy       1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 60

Qy      21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
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Db      61 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 120

Qy      41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 180

Qy      61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 240

Qy      81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 300

Qy     101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 360

Qy     121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
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Db     361 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 420

Qy     141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
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Db     421 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 480

Qy     161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db     481 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 540

Qy     181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
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Db     541 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 600

Qy     201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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Db     601 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 660

Qy     221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Db     661 CAGGCGATTGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 720

Qy     241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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Db     721 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 780

Qy     261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Db     781 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 840

Qy     281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Db     841 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 900

Qy     301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Db     901 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGAGGGATGAAT 960

Qy     321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Db     961 TTGGCTTCATTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1020

Qy     341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Qy     361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Db    1081 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1140

Qy     381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Db    1141 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1200

Qy     401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
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Db    1201 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1260

Qy     421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
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Db    1261 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1320

Qy     441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
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Db    1321 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1380

Qy     461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
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Qy     481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
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Db    1441 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1500

Qy     501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
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Db    1501 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1560

Qy     521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
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Db    1561 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1620

Qy     541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
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Db    1621 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1680

Qy     561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
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Db    1681 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1740

Qy     581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
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Db    1741 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1800

Qy     601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
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Db    1801 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1860

Qy     621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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Db    1861 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 1920

Qy     641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
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Db    1921 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 1980

Qy     661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
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Db    1981 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2040

Qy     681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
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Db       2041 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2100

Qy        701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
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Db       2101 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2160

Qy        721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
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Db       2161 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2220

Qy        741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
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Db       2221 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2280

Qy        761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
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Db       2281 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2340

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
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Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
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Db       2401 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2460

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
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Db       2461 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2520

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
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Db       2521 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2580

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
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Db       2581 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2640

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
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Db       2641 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2700

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2760

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2820

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
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Db       2821 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2880

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
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Db       2881 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 2940

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
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Db       2941 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3000

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
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Db       3001 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3060

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
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Db       3061 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3120

Qy       1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
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Db       3121 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3180

Qy       1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
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Db       3181 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3240

Qy       1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
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Db       3241 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3300

Qy       1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAGATGTCAATCATA 3360

Qy       1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3420

Qy       1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3480

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3540

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3600

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3660

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3720

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3780

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3840

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 3900

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 3960

Qy       1321 PheGluThrAlaLeu 1325
              |||||||||||||||
Db       3961 TTCGAGACAGCACTG 3975
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RESULT 2
US-10-329-258-9
; Sequence 9, Application US/10329258
; Publication No. US20060024233A1
; GENERAL INFORMATION:
; APPLICANT: MUELLER, SABINE
; APPLICANT: GONZALEZ-ZULUETA, MIRELLA
; APPLICANT: FOEHR, ERIK
; APPLICANT: CHIN, DANIEL J.
; TITLE OF INVENTION: USE OF BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZATION OF
; FILE REFERENCE: AGYT-008US2
; CURRENT APPLICATION NUMBER: US/10/329,258
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/343,422
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 29

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;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 4231
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (116)..(4093)
;   OTHER INFORMATION:
US-10-329-258-9

Alignment Scores:
Pred. No.:              0             Length:        4231
Score:                  6779.00       Matches:       1323
Percent Similarity:     99.9%         Conservative:  1
Best Local Similarity:  99.8%         Mismatches:    1
Query Match:            99.9%         Indels:        0
DB:                     7             Gaps:          0

US-09-976-858-42 (1-1325) x US-10-329-258-9 (1-4231)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1015

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1075

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1316 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1375

Qy        421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1376 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1435

Qy        441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1495

Qy        461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1496 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1555

Qy        481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA 1615

Qy        501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1616 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1675

Qy        521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1676 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1735

Qy        541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1736 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1795

Qy        561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1796 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1855

Qy        581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1856 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1915

Qy        601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1916 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 1975

Qy        621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1976 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2035

Qy          641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2036 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2095

Qy          661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2096 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2155

Qy          681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2156 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2215

Qy          701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2216 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2275

Qy          721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2276 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2335

Qy          741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2336 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2395

Qy          761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2396 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2455

Qy          781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2456 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2515

Qy          801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2516 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2575

Qy          821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2635

Qy          841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2636 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2695

Qy          861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2696 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2755

Qy          881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2756 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2815

Qy          901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2816 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2875

Qy          921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2876 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 2935

Qy          941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2936 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 2995

Qy          961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2996 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3055

Qy          981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3056 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3115

Qy         1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3116 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3175

Qy         1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3176 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3235

Qy         1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3236 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3295

Qy         1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3296 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3355

Qy         1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3356 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3415

Qy         1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3416 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3475

Qy         1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db         3476 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG 3535

Qy         1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3536 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3595

Qy         1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3596 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3655

Qy         1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3656 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3715

Qy         1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3716 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG 3775

Qy         1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3776 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3835

Qy         1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3836 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3895

Qy         1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3896 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 3955

Qy         1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4015

Qy         1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         4016 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4075

Qy         1321 PheGluThrAlaLeu 1325
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Db         4076 TTCGAGACAGCACTG 4090
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RESULT 3
US-11-234-786-535
; Sequence 535, Application US/11234786

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; Publication No. US20060024301A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.
;  TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
;  TITLE OF INVENTION:  POLYPEPTIDES THEREOF
;  FILE REFERENCE: 210121.427C31
;  CURRENT APPLICATION NUMBER: US/11/234,786
;  CURRENT FILING DATE:  2005-09-23
;  PRIOR APPLICATION NUMBER: US 09/568,857
;  PRIOR FILING DATE: 2000-05-09
;  PRIOR APPLICATION NUMBER: US 09/536,857
;  PRIOR FILING DATE: 2000-05-27
;  PRIOR APPLICATION NUMBER: US 09/483,672
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: US 09/439,313
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: US 09/352,616
;  PRIOR FILING DATE: 1999-07-13
;  PRIOR APPLICATION NUMBER: US 09/288,946
;  PRIOR FILING DATE: 1999-04-09
;  PRIOR APPLICATION NUMBER: US 09/232,149
;  PRIOR FILING DATE: 1999-01-15
;  PRIOR APPLICATION NUMBER: US 09/159,812
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: US 09/115,453
;  PRIOR FILING DATE: 1998-07-14
;  PRIOR APPLICATION NUMBER: US 09/030,607
;  PRIOR FILING DATE: 1998-02-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 701
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 535
;   LENGTH: 6082
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-234-786-535

Alignment Scores:
Pred. No.:              0             Length:        6082
Score:                  6760.00       Matches:       1324
Percent Similarity:     99.9%         Conservative:  0
Best Local Similarity:  99.9%         Mismatches:    1
Query Match:            99.6%         Indels:        1
DB:                     12            Gaps:          0

US-09-976-858-42 (1-1325) x US-11-234-786-535 (1-6082)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 245

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 305

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 365

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 425

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 485

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 545

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 605

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 665

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 725

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 785

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 845

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 905

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 965

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 1025

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC 1085

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1086 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT 1145

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1205

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1206 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1265

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1266 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1325

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1385

Qy        401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1386 CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT 1445
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Qy    421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
Db   1446 AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG 1505

Qy    441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460
Db   1506 TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG 1565

Qy    461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480
Db   1566 GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG 1625

Qy    481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500
Db   1626 CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAA 1685

Qy    501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520
Db   1686 AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG 1745

Qy    521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540
Db   1746 GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA 1805

Qy    541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560
Db   1806 GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT 1865

Qy    561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580
Db   1866 CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA 1925

Qy    581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600
Db   1926 ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA 1985

Qy    601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620
Db   1986 AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC 2045

Qy    621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGln 640
Db   2046 CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA 2105

Qy    641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660
Db   2106 CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG 2165

Qy    661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlu 680
Db   2166 TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG 2225

Qy    681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700
Db   2226 AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC 2285

Qy    701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720
Db   2286 TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA 2345

Qy    721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740
Db   2346 AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC 2405

Qy    741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760
Db   2406 AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT 2465

Qy    761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
Db   2466 CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA 2525

Qy    781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
Db   2526 GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA 2585

Qy    801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
Db   2586 ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA 2645

Qy    821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
Db   2646 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT 2705

Qy    841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
Db   2706 TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG 2765

Qy    861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
Db   2766 ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA 2825

Qy    881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
Db   2826 TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG 2885

Qy    901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
Db   2886 TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA 2945

Qy    921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
Db   2946 GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG 3005

Qy    941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
Db   3006 TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC 3065

Qy    961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
Db   3066 ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT 3125

Qy    981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
Db   3126 TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT 3185

Qy   1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
Db   3186 GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA 3245

Qy   1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyVal 1040
Db   3246 AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG 3305

Qy   1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
Db   3306 ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT 3365

Qy   1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080
Db   3366 CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA 3425

Qy   1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
Db   3426 AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT 3485

Qy   1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120
Db   3486 GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA 3545

Qy   1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
Db   3546 CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3605

Qy   1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
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Db       3606 CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA 3665

Qy       1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3666 GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA 3725

Qy       1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3726 CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT 3785

Qy       1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db       3786 GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAATC-CGG 3844

Qy       1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3845 GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC 3904

Qy       1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
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Db       3905 AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT 3964

Qy       1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3965 TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA 4024

Qy       1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4025 GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT 4084

Qy       1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
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Db       4085 GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT 4144

Qy       1321 PheGluThrAlaLeu 1325
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Db       4145 TTCGAGACAGCACTG 4159

RESULT 4
US-11-091-883-414
; Sequence 414, Application US/11091883
; Publication No. US20060024693A1
; GENERAL INFORMATION:
;  APPLICANT: CIBELLI, JOSE
;  APPLICANT:  FERNANDEZ, EMILIO O.
;  APPLICANT:  JORDAO DE MEGALHAES, GUILHERME
;  APPLICANT:  KOCABAS, ARIF
;  APPLICANT:  CROSBY, JAVIER A.
;  TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
;  TITLE OF INVENTION:  CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEWBORN
;  TITLE OF INVENTION:  VIABILITY
;  FILE REFERENCE: 53942US
;  CURRENT APPLICATION NUMBER: US/11/091,883
;  CURRENT FILING DATE:  2005-03-29
;  PRIOR APPLICATION NUMBER: 60/556,875
;  PRIOR FILING DATE: 2004-03-29
;  NUMBER OF SEQ ID NOS: 513
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 414
;   LENGTH: 5875
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (988)..(988)
;   OTHER INFORMATION: a, c, g, or t
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (990)..(991)
;   OTHER INFORMATION: a, c, g, or t
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;   NAME/KEY: modified_base
;   LOCATION: (995)..(995)
;   OTHER INFORMATION: a, c, g, or t
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;   NAME/KEY: modified_base
;   LOCATION: (997)..(1000)
;   OTHER INFORMATION: a, c, g, or t
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;   NAME/KEY: modified_base
;   LOCATION: (1003)..(1011)
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;   NAME/KEY: modified_base
;   LOCATION: (1066)..(1066)
;   OTHER INFORMATION: a, c, g, or t
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;   NAME/KEY: modified_base
;   LOCATION: (1321)..(1321)
;   OTHER INFORMATION: a, c, g, or t
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;   NAME/KEY: modified_base
;   LOCATION: (1335)..(1335)
;   OTHER INFORMATION: a, c, g, or t
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;   NAME/KEY: modified_base
;   LOCATION: (3534)..(3534)
;   OTHER INFORMATION: a, c, g, or t
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (3990)..(3990)
;   OTHER INFORMATION: a, c, g, or t
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (4407)..(4407)
;   OTHER INFORMATION: a, c, g, or t
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (4674)..(4674)
;   OTHER INFORMATION: a, c, g, or t
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;   NAME/KEY: modified_base
;   LOCATION: (4790)..(4790)
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;   NAME/KEY: modified_base
;   LOCATION: (4858)..(4858)
;   OTHER INFORMATION: a, c, g, or t
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (4975)..(4975)
;   OTHER INFORMATION: a, c, g, or t
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (5250)..(5250)
;   OTHER INFORMATION: a, c, g, or t
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (5253)..(5253)
;   OTHER INFORMATION: a, c, g, or t
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (5255)..(5257)
;   OTHER INFORMATION: a, c, g, or t
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (5259)..(5259)
;   OTHER INFORMATION: a, c, g, or t
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (5262)..(5262)
;   OTHER INFORMATION: a, c, g, or t
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (5689)..(5689)
;   OTHER INFORMATION: a, c, g, or t
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US-11-091-883-414

Alignment Scores:
Pred. No.:                  0              Length:          5875
Score:                      6686.00        Matches:         1315
Percent Similarity:         99.1%          Conservative:    1
Best Local Similarity:      99.0%          Mismatches:      9
Query Match:                98.5%          Indels:          3
DB:                         12             Gaps:            0

US-09-976-858-42 (1-1325) x US-11-091-883-414 (1-5875)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        116 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA 175

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
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Db        176 CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG 235

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
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Db        236 GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG 295

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
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Db        296 CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA 355

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
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Db        356 ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA 415

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT 475

Qy        121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140
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Db        476 GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG 535

Qy        141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG 595

Qy        161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
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Db        596 TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT 655

Qy        181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
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Db        656 CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT 715

Qy        201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG 775

Qy        221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240
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Db        776 CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG 835

Qy        241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
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Db        836 ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA 895

Qy        261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
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Db        896 CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA 955

Qy        281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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Db        956 ACTGGTATAAGGATAATAAAAATGTACGCCTGNGNNAAGNCNNNNTCNNNNNNNNNTACC 1015

Qy        301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320
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Db       1016 AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGNGGGATGAAT 1075

Qy        321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
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Db       1076 TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG 1135

Qy        341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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Db       1136 CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT 1195

Qy        361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
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Db       1196 GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC 1255

Qy        381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
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Db       1256 GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT 1315

Qy        401 GlnLeu-ProSerAspGly-LysLysMetValHisValGlnAspPheThrAlaPheTrpA 420
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Db       1316 CAGCTNGCCGTCAGATGGTNAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGG 1375

Qy        420 spLysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluL 440
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Db       1376 ATAAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAAT 1435

Qy        440 euLeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuG 460
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Db       1436 TGTTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCG 1495

Qy        460 lyGluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerG 480
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Qy        480 lnGlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrG 500
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Qy        500 luLysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuL 520
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Db       1616 AAAAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGT 1675

Qy        520 euGluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnL 540
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Qy        540 ysAlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspA 560
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Db       1736 AAGCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACG 1795

Qy        560 spProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysG 580
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Db       1796 ATCCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTC 1855

Qy        580 lnIleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaA 600
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Db       1856 AAATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTG 1915

Qy        600 laSerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluP 620
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Db       1916 CAAGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGT 1975

Qy        620 heLeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluG 640
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Db       1976 TCCTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAAC 2035

Qy        640 lnProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValT 660
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Db       2036 AACCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTT 2095

Qy        660 rpSerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrG 680
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Db       2096 GGTCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAG 2155

Qy        680 luAsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnA 700
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Db       2156 AGAATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGG 2215

Qy        700 laTyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuL 720
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Db       2216 CCTATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCC 2275

Qy        720 euAsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaA 740
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Db       2276 TAAACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAA 2335

Qy        740 snLysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuA 760
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Db       2336 ACAAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAG 2395

Qy        760 spLeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyI 780
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Db       2396 ATCTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCA 2455

Qy        780 leAlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnL 800
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Db       2456 TAGCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACA 2515

Qy        800 ysMetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyA 820
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Db       2516 AAATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAA 2575

Qy        820 rgIleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrP 840
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Db       2576 GAATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGT 2635

Qy        840 heLeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaV 860
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Db       2636 TTTTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCG 2695

Qy        860 alIleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgA 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2696 TGATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGC 2755

Qy        880 rgTyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProV 900
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Db       2756 GATATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAG 2815

Qy        900 alPheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaG 920
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Db       2816 TGTTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAG 2875

Qy        920 luGluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheL 940
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Db       2876 AAGAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCT 2935

Qy        940 euPheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheV 960
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Db       2936 TGTTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTG 2995

Qy        960 alIleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValG 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2996 TCATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTG 3055

Qy        980 lyLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnS 1000
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Db       3056 GTTTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAA 3115

Qy       1000 erAlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuG 1020
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Db       3116 GTGCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTG 3175

Qy       1020 luLysGluAlaProTrpGluTyrGlnLysArgProProProAlaTrpProHisGluGlyV 1040
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Db       3176 AAAAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAG 3235

Qy       1040 alIleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysH 1060
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Db       3236 TGATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGC 3295

Qy       1060 isLeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaG 1080
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Db       3296 ATCTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTG 3355

Qy       1080 lyLysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpI 1100
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Db       3356 GAAAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGA 3415

Qy       1100 leAspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleI 1120
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Db       3416 TTGATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCA 3475

Qy       1120 leProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnG 1140
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Db       3476 TACCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAANG 3535

Qy       1140 luHisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleG 1160
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Db       3536 AGCACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTG 3595.

Qy       1160 luAspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValG 1180
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Db       3596 AAGATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTG 3655

Qy       1180 lyGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleI 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3656 GACAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTA 3715

Qy       1200 leAspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleA 1220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3716 TTGATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCC 3775

Qy       1220 rgGluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleA 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3776 GGGAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTG 3835

Qy       1240 spSerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrV 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3836 ACAGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATG 3895

Qy       1260 alLeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaG 1280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3896 TTTTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAG 3955

Qy       1280 luAlaAlaAlaLeuThrGluThrAlaLysGlnVal-TyrPheLysArgAsnTyrProHis 1299
              ||||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db       3956 AAGCCGCTGCCCTCACTGAAACAGCAAAACAGGTNATACTTCAAAAGAAATTATCCACAT 4015

Qy       1300 IleGlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThr 1319
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Db       4016 ATTGGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACT 4075

Qy       1320 IlePheGluThrAlaLeu 1325
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Db       4076 ATTTCGAGACAGCACTG 4093
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RESULT 5
US-11-234-786-536
; Sequence 536, Application US/11234786
; Publication No. US20060024301A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.

```
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.
;  TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
;  TITLE OF INVENTION:  POLYPEPTIDES THEREOF
;  FILE REFERENCE: 210121.427C31
;  CURRENT APPLICATION NUMBER: US/11/234,786
;  CURRENT FILING DATE:  2005-09-23
;  PRIOR APPLICATION NUMBER: US 09/568,857
;  PRIOR FILING DATE: 2000-05-09
;  PRIOR APPLICATION NUMBER: US 09/536,857
;  PRIOR FILING DATE: 2000-05-27
;  PRIOR APPLICATION NUMBER: US 09/483,672
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: US 09/439,313
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: US 09/352,616
;  PRIOR FILING DATE: 1999-07-13
;  PRIOR APPLICATION NUMBER: US 09/288,946
;  PRIOR FILING DATE: 1999-04-09
;  PRIOR APPLICATION NUMBER: US 09/232,149
;  PRIOR FILING DATE: 1999-01-15
;  PRIOR APPLICATION NUMBER: US 09/159,812
;  PRIOR FILING DATE: 1998-09-23
;  PRIOR APPLICATION NUMBER: US 09/115,453
;  PRIOR FILING DATE: 1998-07-14
;  PRIOR APPLICATION NUMBER: US 09/030,607
;  PRIOR FILING DATE: 1998-02-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 701
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 536
;   LENGTH: 6140
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(6140)
;   OTHER INFORMATION: n=A,T,C or G
US-11-234-786-536

Alignment Scores:
Pred. No.:               0            Length:         6140
Score:                   6600.50      Matches:        1300
Percent Similarity:      97.0%        Conservative:   0
Best Local Similarity:   97.0%        Mismatches:     0
Query Match:             97.3%        Indels:         40
DB:                      12           Gaps:           1

US-09-976-858-42 (1-1325) x US-11-234-786-536 (1-6140)

Qy       26 TrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGluGluAspAspMetTyr 45
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      235 TGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAGGAAGATGATATGTAT 294

Qy       46 SerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheTrpAsp 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      295 TCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGGAT 354

Qy       66 LysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArgAlaIleIle 85
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      355 AAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCATA 414

Qy       86 LysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGluGluSerAla 105
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      415 AAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTAATTGAGGAAAGTGCC 474

Qy      106 LysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspPro 125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      475 AAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTTGAAAATTATGATCCC 534

Qy      126 MetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThr 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      535 ATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTGCTGACTTTTTGCACG 594

Qy      146 LeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCysAlaGlyMetArg 165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      595 CTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAGTGTGCTGGGATGAGG 654

Qy      166 LeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsnMetAla 185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      655 TTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGTCTTAGTAACATGGCC 714

Qy      186 MetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsnLysPhe 205
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      715 ATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAATGATGTGAACAAGTTT 774

Qy      206 AspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIleAlaVal 225
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      775 GATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTGCAGGCGATCGCAGTG 834

Qy      226 ThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaValLeuIle 245
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      835 ACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGGATGGCAGTTCTAATC 894

Qy      246 IleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLysThr 265
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      895 ATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCACTGAGGAGTAAAACT 954

Qy      266 AlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIleArgIle 285
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      955 GCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGGTATAAGGATA 1014

Qy      286 IleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArgLysLys 305
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1015 ATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTTGAGAAAGAAG 1074

Qy      306 GluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAlaSerPhePhe 325
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1075 GAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAATTTGGCTTCGTTTTTC 1134

Qy      326 SerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeuGlySerVal 345
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1135 AGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTGTG 1194

Qy      346 IleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaValArgLeuThrVal 365
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1195 ATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCTGTGCGGCTGACGGTT 1254

Qy      366 ThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIleArgArg 385
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1255 ACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATCGTCAGCATCCGAAGA 1314

Qy      386 IleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuProSerAsp 405
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1315 ATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGTCAGCTGCCGTCAGAT 1374

Qy      406 GlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThr 425
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1375 GGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGACC 1434

Qy      426 ProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGly 445
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1435 CCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGCTGTGGTCGGC 1494

Qy      446 ProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSer 465
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1495 CCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATTGGCCCCAAGT 1554

Qy      466 HisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPhe 485
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1555 CACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAGCAGCCCTGGGTGTTC 1614

Qy          486 SerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGlu 505
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1615 TCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAAGGAACGATATGAA 1674

Qy          506 LysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeu 525
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1675 AAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTG 1734

Qy          526 ThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeu 545
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1735 ACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAAGCACGGGTAAACCTT 1794

Qy          546 AlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaVal 565
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1795 GCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGCAGTA 1854

Qy          566 AspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeuHisGluLys 585
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1855 GATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAATTTTGCATGAGAAG 1914

Qy          586 IleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIle 605
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1915 ATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATA 1974

Qy          606 LeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIle 625
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1975 TTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTATA 2034

Qy          626 AspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProProValProGly 645
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2035 GATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAGGA 2094

Qy          646 ThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGlnGlnSerSer 665
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2095 ACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCT 2154

Qy          666 ArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnValProValThr 685
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2155 AGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAGAATGTCCCAGTTACA 2214

Qy          686 LeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTyrLysAsnTyrPhe 705
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2215 CTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCTATAAGAATTACTTC 2274

Qy          706 ArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAlaAlaGln 725
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2275 AGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTAAACACTGCAGCTCAG 2334

Qy          726 ValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMetLeu 745
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2335 GTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAACAAACAAAGTATGCTA 2394

Qy          746 AsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsnTrpTyrLeu 765
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2395 AATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAACTGGTACTTA 2454

Qy          766 GlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeu 785
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2455 GGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATAGCAAGATCTCTATTG 2514

Qy          786 ValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIle 805
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2515 GTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAAATGTTTGAGTCAATT 2574

Qy          806 LeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArgPhe 825
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2575 CTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTTAAATCGTTTC 2634

Qy          826 SerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGln 845
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2635 TCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTTTTAGATTTCATCCAG 2694

Qy          846 ThrLeuLeuGlnValValGlyValValSerValAlaValAlaValIleProTrpIleAla 865
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2695 ACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCGCA 2754

Qy          866 IleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGluThr 885
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2755 ATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGATATTTTTTGGAAACG 2814

Qy          886 SerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSerHisLeuSer 905
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2815 TCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGTCA 2874

Qy          906 SerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArgCysGlnGlu 925
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2875 TCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAAGAGAGGTGTCAGGAA 2934

Qy          926 LeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSer 945
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2935 CTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTGTTTTTGACAACGTCC 2994

Qy          946 ArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPhe 965
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2995 CGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTCATCATCGTTGCCTTT 3054

Qy          966 GlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyr 985
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3055 GGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGTTTGGCACTGTCCTAT 3114

Qy          986 AlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGluValGluAsn 1005
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3115 GCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGTGCTGAAGTTGAGAAT 3174

Qy         1006 MetMetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGluAlaProTrp 1025
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3175 ATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAAAAAGAAGCACCTTGG 3234

Qy         1026 GluTyrGlnLysArgProProProAlaTrpProHisGluGlyValIleIlePheAspAsn 1045
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3235 GAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTGATAATCTTTGACAAT 3294

Qy         1046 ValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIle 1065
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3295 GTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCATCTGACAGCACTCATT 3354

Qy         1066 LysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeuIle 1085
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3355 AAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATC 3414

Qy         1086 SerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIleAspLysIleLeuThr 1105
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3415 TCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATTGATAAGATCTTGACA 3474

Qy         1106 ThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGluProVal 1125
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3475 ACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTGTT 3534

Qy         1126 LeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThrAspGluGlu 1145
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3535 TTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAATGAGCACACGGATGAGGAA 3594

Qy         1146 LeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLys 1165
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3595 CTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAAGATCTTCCTGGTAAA 3654

Qy         1166 MetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGlnArgGlnLeuVal 1185
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3655 ATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGACAAAGACAACTGGTG 3714

Qy         1186 CysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAlaThrAla 1205
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3715 TGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATTGATGAAGCGACGGCA 3774
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Qy       1206 AsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPheAlaHis 1225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3775 AATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGGGAGAAATTTGCCCAC 3834

Qy       1226 CysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLysIleMet 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3835 TGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGACAGCGACAAGATAATG 3894

Qy       1246 ValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGlnAsnLys 1265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3895 GTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTTTTGCTGCAAAATAAA 3954

Qy       1266 GluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGluAlaAlaAlaLeuThr 1285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3955 GAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAAGCCGCTGCCCTCACT 4014

Qy       1286 GluThrAlaLysGln--------------------------------------------- 1290
              |||||||||||||||
Db       4015 GAAACAGCAAAACAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGA 4074

Qy       1290 ------------------------------------------------------------ 1290

Db       4075 CCTCAAGTGATCCACCTGCCTTGGCCTCCCAAACTGCTGAGATTACAGGTGTGAGCCACC 4134

Qy       1291 ------------ValTyrPheLysArgAsnTyrProHisIleGlyHisThrAspHisMe 1306
                          ||||||||||||||||||||||||||||||||||||||||||||||||
Db       4135 ACGCCCAGCCTGAGTATACTTCAAAAGAAATTATCCACATATTGGTCACACTGACCACAT 4194

Qy       1306 tValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIlePheGluThrAlaLeu 1325
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4195 GGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATTTCGAGACAGCACTG 4252

RESULT 6
US-11-124-367A-150
; Sequence 150, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
;  APPLICANT: Michele Cargill
;  APPLICANT:  Hongjin Huang
;  TITLE OF INVENTION: Genetic Polymorphisms Associated with
;  TITLE OF INVENTION:  Fibrosis Methods of Detection and Uses Thereof
;  FILE REFERENCE: CL001519.ORD
;  CURRENT APPLICATION NUMBER: US/11/124,367A
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US 60/568,846
;  PRIOR FILING DATE: 2004-05-07
;  PRIOR APPLICATION NUMBER: US 60/582,609
;  PRIOR FILING DATE: 2004-06-25
;  PRIOR APPLICATION NUMBER: US 60/599,554
;  PRIOR FILING DATE: 2004-08-09
;  NUMBER OF SEQ ID NOS: 34460
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 150
;   LENGTH: 2143
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-124-367A-150

Alignment Scores:
Pred. No.:              1.05e-308     Length:        2143
Score:                  3310.50       Matches:       656
Percent Similarity:     92.8%         Conservative:  0
Best Local Similarity:  92.8%         Mismatches:    0
Query Match:            48.8%         Indels:        51
DB:                     12            Gaps:          1

US-09-976-858-42 (1-1325) x US-11-124-367A-150 (1-2143)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         22 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 81

Qy         21 ArgValPhePheTrp--------------------------------------------- 25
              |||||||||||||||
Db         82 CGCGTGTTCTTCTGGTCTCCCCCGCCTCTTTCTTGGAAGGACACTTGCCATTGGATTTAG 141

Qy         25 ------------------------------------------------------------ 25

Db        142 GACCCACTTGGATAATCCAGGATGATGTCTTCACTCCAACATCCTCAGTTTAATTCCATG 201

Qy         26 ------------------------------------------------TrpLeuAsnPro 29
                                                              ||||||||||||
Db        202 TGCAAATACCCTTTTCCCAAATAACATTCAATTCTTTACCAGGAAAGGTGGCTCAATCCC 261

Qy         30 LeuPheLysIleGlyHisLysArgArgLeuGluGluAspAspMetTyrSerValLeuPro 49
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 TTGTTTAAAATTGGCCATAAACGGAGATTAGAGGAAGATGATATGTATTCAGTGCTGCCA 321

Qy         50 GluAspArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheTrpAspLysGluValLeu 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 GAAGACCGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGGATAAAGAAGTTTTA 381

Qy         70 ArgAlaGluAsnAspAlaGlnLysProSerLeuThrArgAlaIleIleLysCysTyrTrp 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 AGAGCTGAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCATAAAGTGTTACTGG 441

Qy         90 LysSerTyrLeuValLeuGlyIlePheThrLeuIleGluGluSerAlaLysValIleGln 109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 AAATCTTATTTAGTTTTGGGAATTTTTACGTTAATTGAGGAAAGTGCCAAAGTAATCCAG 501

Qy        110 ProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspProMetAspSerVal 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 CCCATATTTTTGGGAAAAATTATTAATTATTTTGAAAATTATGATCCCATGGATTCTGTG 561

Qy        130 AlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThrLeuIleLeuAla 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 GCTTTGAACACAGCGTACGCCTATGCCACGGTGCTGACTTTTTGCACGCTCATTTTGGCT 621

Qy        150 IleLeuHisHisLeuTyrPheTyrHisValGlnCysAlaGlyMetArgLeuArgValAla 169
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 ATACTGCATCACTTATATTTTTATCACGTTCAGTGTGCTGGGATGAGGTTACGAGTAGCC 681

Qy        170 MetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsnMetAlaMetGlyLysThr 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 ATGTGCCATATGATTTATCGGAAGGCACTTCGTCTTAGTAACATGGCCATGGGGAAGACA 741

Qy        190 ThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsnLysPheAspGlnValThr 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 ACCACAGGCCAGATAGTCAATCTGCTGTCCAATGATGTGAACAAGTTTGATCAGGTGACA 801

Qy        210 ValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIleAlaValThrAlaLeuLeu 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 GTGTTCTTACACTTCCTGTGGGCAGGACCACTGCAGGCGATTGCAGTGACTGCCCTACTC 861

Qy        230 TrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaValLeuIleIleLeuLeuPro 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 TGGATGGAGATAGGAATATCGTGCCTTGCTGGGATGGCAGTTCTAATCATTCTCCTGCCC 921

Qy        250 LeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLysThrAlaThrPheThr 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 TTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCACTGAGGAGTAAAACTGCAACTTTCACG 981

Qy        270 AspAlaArgIleArgThrMetAsnGluValIleThrGlyIleArgIleIleLysMetTyr 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 GATGCCAGGATCAGGACCATGAATGAAGTTATAACTGGTATAAGGATAATAAAAATGTAC 1041

Qy        290 AlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArgLysLysGluIleSerLys 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 GCCTGGGAAAAGTCATTTTCAAATCTTATTACCAATTTGAGAAAGAAGGAGATTTCCAAG 1101

Qy        310 IleLeuArgSerSerCysLeuArgGlyMetAsnLeuAlaSerPhePheSerAlaSerLys 329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 ATTCTGAGAAGTTCCTGCCTCAGAGGGATGAATTTGGCTTCATTTTTCAGTGCAAGCAAA 1161

Qy        330 IleIleValPheValThrPheThrThrTyrValLeuLeuGlySerValIleThrAlaSer 349
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1162 ATCATCGTGTTTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTGTGATCACAGCCAGC 1221

Qy        350 ArgValPheValAlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePhe 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1222 CGCGTGTTCGTGGCAGTGACGCTGTATGGGGCTGTGCGGCTGACGGTTACCCTCTTCTTC 1281

Qy        370 ProSerAlaIleGluArgValSerGluAlaIleValSerIleArgArgIleGlnThrPhe 389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1282 CCCTCAGCCATTGAGAGGGTGTCAGAGGCAATCGTCAGCATCCGAAGAATCCAGACCTTT 1341

Qy        390 LeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuProSerAspGlyLysLysMet 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1342 TTGCTACTTGATGAGATATCACAGCGCAACCGTCAGCTGCCGTCAGATGGTAAAAAGATG 1401

Qy        410 ValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThrProThrLeuGln 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1402 GTGCATGTGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGACCCCAACTCTACAA 1461

Qy        430 GlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGlyProValGlyAla 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1462 GGCCTTTCCTTTACTGTCAGACCTGGCGAATTGTTAGCTGTGGTCGGCCCCGTGGGAGCA 1521

Qy        450 GlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHisGlyLeuVal 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1522 GGGAAGTCATCACTGTTAAGTGCCGTGCTCGGGGAATTGGCCCCAAGTCACGGGCTGGTC 1581

Qy        470 SerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPheSerGlyThrLeu 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1582 AGCGTGCATGGAAGAATTGCCTATGTGTCTCAGCAGCCCTGGGTGTTCTCGGGAACTCTG 1641

Qy        490 ArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGluLysValIleLys 509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1642 AGGAGTAATATTTTATTTGGGAAGAAATACGAAAAGGAACGATATGAAAAAGTCATAAAG 1701

Qy        510 AlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThrValIleGly 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1702 GCTTGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTGACTGTGATAGGA 1761

Qy        530 AspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAlaVal 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1762 GATCGGGGAACCACGCTGAGTGGAGGGCAGAAAGCACGGGTAAACCTTGCAAGAGCAGTG 1821

Qy        550 TyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGluVal 569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1822 TATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGCAGTAGATGCGGAAGTT 1881

Qy        570 SerArgHisLeuPheGluLeuCysIleCysGlnIleLeuHisGluLysIleThrIleLeu 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1882 AGCAGACACTTGTTCGAACTGTGTATTTGTCAAATTTTGCATGAGAAGATCACAATTTTA 1941

Qy        590 ValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIleLeuLysAspGly 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1942 GTGACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATATTGAAAGATGGT 2001

Qy        610 LysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIleAspPheGlySer 629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2002 AAAATGGTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTATAGATTTTGGCTCC 2061

Qy        630 LeuLeuLysLysAspAsnGluGluSerGluGlnProProValProGlyThrProThrLeu 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2062 CTTTTAAAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAGGAACTCCCACACTA 2121

Qy        650 ArgAsnArgThrPheSerGlu 656
              |||||||||||||||||||||
Db       2122 AGGAATCGTACCTTCTCAGAG 2142
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RESULT 7
US-11-124-367A-148
; Sequence 148, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 2256
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-124-367A-148

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Alignment Scores:
Pred. No.:               5.42e-304     Length:         2256
Score:                   3262.00       Matches:        655
Percent Similarity:      87.9%         Conservative:   0
Best Local Similarity:   87.9%         Mismatches:     1
Query Match:             48.1%         Indels:         90
DB:                      12            Gaps:           1

US-09-976-858-42 (1-1325) x US-11-124-367A-148 (1-2256)

Qy          1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         22 ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACCTCTGCTCA 81

Qy         21 ArgValPhePheTrp--------------------------------------------- 25
              |||||||||||||
Db         82 CGCGTGTTCTTCTG-ATGGAGTCTCGCTGTGTCACCCAGGCTGGAGTGCAGTGGCGCAGT 140

Qy         25 ------------------------------------------------------------ 25

Db        141 CTCAGCTCACTGCAGCCTCCACCTCCTGTGTTCAAGCAGTCCTCCTGCCTCAGCCACCAG 200

Qy         25 ------------------------------------------------------------ 25

Db        201 ACTAGCAGGTCTCCCCCGCCTCTTTCTTGGAAGGACACTTGCCATTGGATTTAGGACCCA 260

Qy         25 ------------------------------------------------------------ 25

Db        261 CTTGGATAATCCAGGATGATGTCTTCACTCCAACATCCTCAGTTTAATTCCATGTGCAAA 320

Qy         26 ------------------------------------------TrpLeuAsnProLeuPhe 31
                                                        ||||||||||||||||||
Db        321 TACCCTTTTCCCAAATAACATTCAATTCTTTACCAGGAAAGGTGGCTCAATCCCTTGTTT 380

Qy         32 LysIleGlyHisLysArgArgLeuGluGluAspAspMetTyrSerValLeuProGluAsp 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAAATTGGCCATAAACGGAGATTAGAGGAAGATGATATGTATTCAGTGCTGCCAGAAGAC 440

Qy         52 ArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheTrpAspLysGluValLeuArgAla 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 CGCTCACAGCACCTTGGAGAGGAGTTGCAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCT 500

Qy         72 GluAsnAspAlaGlnLysProSerLeuThrArgAlaIleIleLysCysTyrTrpLysSer 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GAGAATGACGCACAGAAGCCTTCTTTAACAAGAGCAATCATAAAGTGTTACTGGAAATCT 560

Qy         92 TyrLeuValLeuGlyIlePheThrLeuIleGluGluSerAlaLysValIleGlnProIle 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TATTTAGTTTTGGGAATTTTTACGTTAATTGAGGAAAGTGCCAAAGTAATCCAGCCCATA 620

Qy        112 PheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspProMetAspSerValAlaLeu 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TTTTGGGAAAAATTATTAATTATTTTGAAAATTATGATCCCATGGATTCTGTGGCTTTG 680
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Qy        132 AsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThrLeuIleLeuAlaIleLeu 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 AACACAGCGTACGCCTATGCCACGGTGCTGACTTTTGCACGCTCATTTTGGCTATACTG 740

Qy        152 HisHisLeuTyrPheTyrHisValGlnCysAlaGlyMetArgLeuArgValAlaMetCys 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 CATCACTTATATTTTTATCACGTTCAGTGTGCTGGGATGAGGTTACGAGTAGCCATGTGC 800

Qy        172 HisMetIleTyrArgLysAlaLeuArgLeuSerAsnMetAlaMetGlyLysThrThrThr 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 CATATGATTTATCGGAAGGCACTTCGTCTTAGTAACATGGCCATGGGGAAGACAACCACA 860

Qy        192 GlyGlnIleValAsnLeuLeuSerAsnAspValAsnLysPheAspGlnValThrValPhe 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGCCAGATAGTCAATCTGCTGTCCAATGATGTGAACAAGTTTGATCAGGTGACAGTGTTC 920

Qy        212 LeuHisPheLeuTrpAlaGlyProLeuGlnAlaIleAlaValThrAlaLeuLeuTrpMet 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 TTACACTTCCTGTGGGCAGGACCACTGCAGGCGATTGCAGTGACTGCCCTACTCTGGATG 980

Qy        232 GluIleGlyIleSerCysLeuAlaGlyMetAlaValLeuIleIleLeuLeuProLeuGln 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 GAGATAGGAATATCGTGCCTTGCTGGGATGGCAGTTCTAATCATTCTCCTGCCCTTGCAA 1040

Qy        252 SerCysPheGlyLysLeuPheSerSerLeuArgSerLysThrAlaThrPheThrAspAla 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1041 AGCTGTTTTGGGAAGTTGTTCTCATCACTGAGGAGTAAAACTGCAACTTTCACGGATGCC 1100

Qy        272 ArgIleArgThrMetAsnGluValIleThrGlyIleArgIleIleLysMetTyrAlaTrp 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1101 AGGATCAGGACCATGAATGAAGTTATAACTGGTATAAGGATAATAAAAATGTACGCCTGG 1160

Qy        292 GluLysSerPheSerAsnLeuIleThrAsnLeuArgLysLysGluIleSerLysIleLeu 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1161 GAAAAGTCATTTTCAAATCTTATTACCAATTTGAGAAAGAAGGAGATTTCCAAGATTCTG 1220

Qy        312 ArgSerSerCysLeuArgGlyMetAsnLeuAlaSerPhePheSerAlaSerLysIleIle 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1221 AGAAGTTCCTGCCTCAGAGGGATGAATTTGGCTTCATTTTTCAGTGCAAGCAAAATCATC 1280

Qy        332 ValPheValThrPheThrThrTyrValLeuLeuGlySerValIleThrAlaSerArgVal 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1281 GTGTTTGTGACCTTCACCACCTACGTGCTCCTCGGCAGTGTGATCACAGCCAGCCGCGTG 1340

Qy        352 PheValAlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePheProSer 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1341 TTCGTGGCAGTGACGCTGTATGGGGCTGTGCGGCTGACGGTTACCCTCTTCTTCCCCTCA 1400

Qy        372 AlaIleGluArgValSerGluAlaIleValSerIleArgArgIleGlnThrPheLeuLeu 391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1401 GCCATTGAGAGGGTGTCAGAGGCAATCGTCAGCATCCGAAGAATCCAGACCTTTTTGCTA 1460

Qy        392 LeuAspGluIleSerGlnArgAsnArgGlnLeuProSerAspGlyLysLysMetValHis 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1461 CTTGATGAGATATCACAGCGCAACCGTCAGCTGCCGTCAGATGGTAAAAAGATGGTGCAT 1520

Qy        412 ValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThrProThrLeuGlnGlyLeu 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1521 GTGCAGGATTTTACTGCTTTTTGGGATAAGGCATCAGAGACCCCAACTCTACAAGGCCTT 1580

Qy        432 SerPheThrValArgProGlyGluLeuLeuAlaValValGlyProValGlyAlaGlyLys 451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1581 TCCTTTACTGTCAGACCTGGCGAATTGTTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAG 1640

Qy        452 SerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHisGlyLeuValSerVal 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1641 TCATCACTGTTAAGTGCCGTGCTCGGGGAATTGGCCCCAAGTCACGGGCTGGTCAGCGTG 1700

Qy        472 HisGlyArgIleAlaTyrValSerGlnGlnProTrpValPheSerGlyThrLeuArgSer 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1701 CATGGAAGAATTGCCTATGTGTCTCAGCAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGT 1760

Qy        492 AsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGluLysValIleLysAlaCys 511
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1761 AATATTTTATTTGGGAAGAAATACGAAAAGGAACGATATGAAAAAGTCATAAAGGCTTGT 1820

Qy        512 AlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThrValIleGlyAspArg 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1821 GCTCTGAAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTGACTGTGATAGGAGATCGG 1880

Qy        532 GlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAlaValTyrGln 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1881 GGAACCACGCTGAGTGGAGGGCAGAAAGCACGGGTAAACCTTGCAAGAGCAGTGTATCAA 1940

Qy        552 AspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGluValSerArg 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1941 GATGCTGACATCTATCTCCTGGACGATCCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGA 2000

Qy        572 HisLeuPheGluLeuCysIleCysGlnIleLeuHisGluLysIleThrIleLeuValThr 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2001 CACTTGTTCGAACTGTGTATTTGTCAAATTTTGCATGAGAAGATCACAATTTTAGTGACT 2060

Qy        592 HisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIleLeuLysAspGlyLysMet 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2061 CATCAGTTGCAGTACCTCAAAGCTGCAAGTCAGATTCTGATATTGAAAGATGGTAAAATG 2120

Qy        612 ValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIleAspPheGlySerLeuLeu 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2121 GTGCAGAAGGGGACTTACACTGAGTTCCTAAAATCTGGTATAGATTTTGGCTCCCTTTTA 2180

Qy        632 LysLysAspAsnGluGluSerGluGlnProProValProGlyThrProThrLeuArgAsn 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2181 AAGAAGGATAATGAGGAAAGTGAACAACCTCCAGTTCCAGGAACTCCCACACTAAGGAAT 2240

Qy        652 ArgThrPheSerGlu 656
              |||||||||||||||
Db       2241 CGTACCTTCTCAGAG 2255
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RESULT 8
US-10-826-585-35
; Sequence 35, Application US/10826585
; Publication No. US20060008807A1
; GENERAL INFORMATION:
; APPLICANT: Immunivest Corporation
; APPLICANT: O'Hara, Shawn Mark
; APPLICANT: Foulk, Brad
; APPLICANT: Zweitzig, Daniel
; TITLE OF INVENTION: Multiparameter analysis of comprehensive nucleic acids and
; TITLE OF INVENTION: morphological features on the same sample
; FILE REFERENCE: IMMC 143 PCT/US
; CURRENT APPLICATION NUMBER: US/10/826,585
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 60/369945
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/330669
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US02/26867
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 5011
; TYPE: DNA
; ORGANISM: Human
US-10-826-585-35

Alignment Scores:

Pred. No.:	2.81e-209	Length:	5011
Score:	2285.50	Matches:	528
Percent Similarity:	56.6%	Conservative:	274
Best Local Similarity:	37.3%	Mismatches:	491
Query Match:	33.7%	Indels:	124
DB:	7	Gaps:	30

US-09-976-858-42 (1-1325) x US-10-826-585-35 (1-5011)

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Qy          3 ProValTyrGlnGluVal------LysProAsnProLeuGlnAsp------AlaAsnLeu 18
Db        782 CCCCTGTTCTCGGAAACCATCCACGACCCTAATCCCTGCCCAGAGTCCAGCGCTTCCTTC 841

Qy         19 CysSerArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArg 38
Db        842 CTGTCGAGGATCACCTTCTGGTGGATCACAGGGTTGATTGTCCGGGGCTACCGCCAGCCC 901

Qy         39 LeuGluGluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGlu 58
Db        902 CTGGAGGGCAGTGACCTCTGGTCCTTAAACAAGGAGGACACGTCGGAACAAGTCGTGCCT 961

Qy         59 GluLeuGlnGlyPheTrpAspLysGlu--------------------------------- 67
Db        962 GTTTTGGTAAAGAACTGGAAGAAGGAATGCGCCAAGACTAGGAAGCAGCCGGTGAAGGTT 1021

Qy         68 ValLeuArgAlaGluAsnAspAlaGln--------------------------------- 76
Db       1022 GTGTACTCCTCCAAGGATCCTGCCCAGCCGAAAGAGAGTTCCAAGGTGGATGCGAATGAG 1081

Qy         77 ------------------------------------------LysProSerLeuThrArg 82
Db       1082 GAGGTGGAGGCTTTGATCGTCAAGTCCCCACAGAAGGAGTGGAACCCCTCTCTGTTTAAG 1141

Qy         83 AlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGlu 102
Db       1142 GTGTTATACAAGACCTTTGGGCCCTACTTCCTCATGAGCTTCTTCTTCAAGGCCATCCAC 1201

Qy        103 GluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsn 122
Db       1202 GACCTGATGATGTTTTCCGGGCCGCAGATCTTA---AAGTTGCTCATCAAGTTCGTGAAT 1258

Qy        123 TyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThr 142
Db       1259 ------------GACACGAAGGCCCCAGACTGGCAGGGCTACTTCTACACCGTGCTGCTG 1306

Qy        143 PheCysThrLeuIleLeu---AlaIleLeuHisHisLeuTyrPheTyrHisValGlnCys 161
Db       1307 TTTGTCACTGCCTGCCTGCAGACCCTCGTGCTGCACCAGTACTTCCACATCTGCTTCGTC 1366

Qy        162 AlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeu 181
Db       1367 AGTGGCATGAGGATCAAGACCGCTGTCATTGGGGCTGTCTATCGGAAGGCCCTGGTGATC 1426

Qy        182 SerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAsp 201
Db       1427 ACCAATTCAGCCAGAAAATCCTCCACGGTCGGGGAGATTGTCAACCTCATGTCTGTGGAC 1486

Qy        202 ValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGln 221
Db       1487 GCTCAGAGGTTCATGGACTTGGCCACGTACATTAACATGATCTGGTCAGCCCCCCTGCAA 1546

Qy        222 AlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMet 241
Db       1547 GTCATCCTTGCTCTCTACCTCCTGTGGCTGAATCTGGGCCCTTCCGTCCTGGCTGGAGTG 1606

Qy        242 AlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeu 261
Db       1607 GCGGTGATGGTCCTCATGGTGCCCGTCAATGCTGTG---------------------ATG 1645

Qy        262 ArgSerLysThrAlaThrPhe---------------------ThrAspAlaArgIleArg 274
Db       1646 GCGATGAAGACCAAGACGTATCAGGTGGCCCACATGAAGAGCAAAGACAATCGGATCAAG 1705

Qy        275 ThrMetAsnGluValIleThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSer 294
Db       1706 CTGATGAACGAAATTCTCAATGGGATCAAAGTGCTAAAGCTTTATGCCTGGGAGCTGGCA 1765

Qy        295 PheSerAsnLeuIleThrAsnLeuArgLysLysGluIleSerLysIleLeuArgSerSer 314
Db       1766 TTCAAGGACAAGGTGCTGGCCATCAGGCAGGAGGAGCTGAAGGTGCTGAAGAAGTCTGCC 1825

Qy        315 CysLeuArgGlyMetAsnLeuAlaSerPhePheSerAlaSerLysIleIleValPheVal 334
Db       1826 TACCTGTCAGCCGTGGGCACCTTCACCTGGGTCTGCACGCCCTTTCTGGTGGCCTTGTGC 1885

Qy        335 ThrPheThrThrTyrValLeuLeu------GlySerValIleThrAlaSerArgValPhe 352
Db       1886 ACATTTGCCGTCTACGTGACCATTGACGAGAACAACATCCTGGATGCCCAGACAGCCTTC 1945

Qy        353 ValAlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePheProSerAla 372
Db       1946 GTGTCTTTGGCCTTGTTCAACATCCTCCGGTTTCCCCTGAACATT---CTCCCCATGGTC 2002

Qy        373 IleGluArgValSerGluAlaIleValSerIleArgArgIleGlnThrPheLeuLeuLeu 392
Db       2003 ATCAGCAGCATCGTGCAGGCGAGTGTCTCCCTCAAACGCCTGAGGATCTTTCTCTCCCAT 2062.

Qy        393 AspGluIleSer------------GlnArgAsnArgGlnLeuProSerAspGlyLysLys 408
Db       2063 GAGGAGCTGGAACCTGACAGCATCGAGCGACGGCCTGTCAAAGACGGCGGGGGCACGAAC 2122

Qy        409 MetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThrProThrLeu 428
Db       2123 AGCATCACCGTGAGGAATGCCACATTCACCTGGGCCAGG---AGCGACCCTCCCACACTG 2179

Qy        429 GlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGlyProValGly 448
Db       2180 AATGGCATCACCTTCTCCATCCCCGAAGGTGCTTTGGTGGCCGTGGTGGGCCAGGTGGGC 2239

Qy        449 AlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHisGlyLeu 468
Db       2240 TGCGGAAAGTCGTCCCTGCTCTCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCAC 2299

Qy        469 ValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPheSerGlyThr 488
Db       2300 GTGGCTATCAAGGGCTCCGTGGCCTATGTGCCACAGCAGGCCTGGATTCAGAATGATTCT 2359

Qy        489 LeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGluLysValIle 508
Db       2360 CTCCGAGAAAACATCCTTTTTGGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATA 2419

Qy        509 LysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThrValIle 528
Db       2420 CAGGCCTGTGCCCTCCTCCCAGACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGATT 2479

Qy        529 GlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAla 548
Db       2480 GGCGAGAAGGGCGTGAACCTGTCTGGGGGCCAGAAGCAGCGCGTGAGCCTGGCCCGGGCC 2539

Qy        549 ValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGlu 568
Db       2540 GTGTACTCCAACGCTGACATTTACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCCCAT 2599.

Qy        569 ValSerArgHisLeuPheGluLeuCysIleCysGln------IleLeuHisGluLysIle 586
Db       2600 GTGGGAAAACACATCTTTGAAAATGTGATTGGCCCCAAGGGGATGCTGAAGAACAAGACG 2659

Qy        587 ThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIleLeu 606
Db       2660 CGGATCTTGGTCACGCACAGCATGAGCTACTTGCCGCAGGTGGACGTCATCATCGTCATG 2719

Qy        607 LysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIleAsp 626
Db       2720 AGTGGCGGCAAGATCTCTGAGATGGGCTCCTACCAGGAGCTGCTGGCTCGAGACGGCGCC 2779

Qy        627 PheGlySerLeuLeuLys-----------------------LysAspAsnGluGluSer 638
Db       2780 TTCGCTGAGTTCCTGCGTACCTATGCCAGCACAGAGCAGGAGCAGGATGCAGAGGAGAAC 2839

Qy        639 GluGlnProProValProGly------------ThrProThrLeuArgAsn--------- 651
Db       2840 GGGGTCACGGGCGTCAGCGGTCCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCATGCTG 2899

Qy        652 -----------------------------ArgThrPheSerGluSerSerValTrpSer 661
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Db       2900 GTGACGGACAGTGCAGGGAAGCAACTGCAGAGACAGCTCAGCAGCTCCTCCTCCTATAGT 2959
Qy        662 GlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsn 681
Db       2960 GGGGACATCAGCAGGCACCACAACAGCACCGCAGAACTGCAGAAAGCTGAGGCCAAGAAG 3019
Qy        682 ValProVal---ThrLeuSerGluGluAsnArgSerGlu---GlyLysValGlyPheGln 699
Db       3020 GAGGAGACCTGGAAGCTGATGGAGGCTGACAAGGCGCAGACAGGGCAGGTCAAGCTTTCC 3079
Qy        700 AlaTyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPhe------IlePheLeu 717
Db       3080 GTGTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTCCTTCCTCAGCATCTTCCTT 3139
Qy        718 IleLeuLeuAsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyr 737
Db       3140 TTCATGTGTAAC---------CATGTGTCCGCGCTGGCTTCCAACTATTGGCTCAGCCTC 3190
Qy        738 TrpAlaAsnLysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGlu 757
Db       3191 TGGACTGAT---------------GACCCCATCGTCAACGGGACTCAGGAGCACACGAAA 3235
Qy        758 ---LysLeuAspLeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrVal 776
Db       3236 GTCCGGCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATCGCCGTG--------- 3286
Qy        777 LeuPheGlyIleAlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThr 796
Db       3287 ---TTTGGCTACTCCATGGCCGTGTCCATCGGGGGGATCTTG------GCTTCCCGCTGT 3337
Qy        797 LeuHisAsnLysMetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsn 816
Db       3338 CTGCACGTGGACCTGCTGCACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACC 3397
Qy        817 ProIleGlyArgIleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeu 836
Db       3398 CCCAGTGGGAACCTGGTGAACCGCTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATC 3457
Qy        837 ProLeuThrPheLeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerVal 856
Db       3458 CCGGAGGTCATCAAGATGTTCATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTT 3517
Qy        857 AlaValAlaValIleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIle 876
Db       3518 ATCCTGCTGGCCACGCCCATCGCCGCCATCATCATCCCGCCCCTTGGCCTCATCTACTTC 3577
Qy        877 PheLeuArgArgTyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThr 896
Db       3578 TTCGTCCAGAGGTTCTACGTGGCTTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGC 3637
Qy        897 ArgSerProValPheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAla 916
Db       3638 CGCTCCCCGGTCTATTCCCATTTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCC 3697
Qy        917 TyrLysAlaGluGluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGlu 936
Db       3698 TTCGAGGAGCAGGAGCGCTTCATCCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAG 3757
Qy        937 AlaTrpPheLeuPheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCys 956
Db       3758 GCCTATTACCCCAGCATCGTGGCCAACAGGTGGCTGGCCGTGCGGCTGGAGTGTGTGGGC 3817
Qy        957 AlaMetPheValIleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAla 976
Db       3818 AACTGCATCGTTCTGTTTGCTGCCCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCT 3877
Qy        977 GlyGlnValGlyLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCys 996
Db       3878 GGCTTGGTGGGCCTCTCAGTGTCTTACTCATTGCAGGTCACCACGTACTTGAACTGGCTG 3937
Qy        997 ValArgGlnSerAlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyr 1016
Db       3938 GTTCGGATGTCATCTGAAATGGAAACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTAT 3997
Qy       1017 ThrAspLeuGluLysGluAlaProTrpGluTyrGlnLys---ArgProProProAlaTrp 1035
Db       3998 TCAGAGACTGAGAAGGAGGCGCCCTGGCAAATCCAGGAGACAGCTCCGCCCAGCAGCTGG 4057
Qy       1036 ProHisGluGlyValIleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyPro 1055
Db       4058 CCCCAGGTGGGCCGAGTGGAATTCCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGAC 4117
Qy       1056 LeuValLeuLysHisLeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGly 1075
Db       4118 TTCGTTCTCAGGCACATCAATGTCACGATCAATGGGGGAGAAAAGGTCGGCATCGTGGGG 4177
Qy       1076 ArgThrGlyAlaGlyLysSerSerLeuIleSerAlaLeuPheArgLeuSerGlu---Pro 1094
Db       4178 CGGACGGGAGCTGGGAAGTCGTCCCTGACCCTGGGCTTATTTCGGATCAACGAGTCTGCC 4237
Qy       1095 GluGlyLysIleTrpIleAspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArg 1114
Db       4238 GAAGGAGAGATCATCATCGATGGCATCAACATCGCCAAGATCGGCCTGCACGACCTCCGC 4297
Qy       1115 LysLysMetSerIleIleProGlnGluProValLeuPheThrGlyThrMetArgLysAsn 1134
Db       4298 TTCAAGATCACCATCATCCCCCAGGACCCTGTTTTGTTTTCGGGTTCCCTCCGAATGAAC 4357
Qy       1135 LeuAspProPheAsnGluHisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGln 1154
Db       4358 CTGGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCAC 4417
Qy       1155 LeuLysGluThrIleGluAspLeuProGlyLysMetAspThrGluLeuAlaGluSerGly 1174
Db       4418 CTGAAGGACTTCGTGTCAGCCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGG 4477
Qy       1175 SerAsnPheSerValGlyGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLys 1194
Db       4478 GAGAACCTCAGTGTCGGGCAGCGCCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAAG 4537
Qy       1195 AsnGlnIleLeuIleIleAspGluAlaThrAlaAsnValAspProArgThrAspGluLeu 1214
Db       4538 ACGAAGATCCTTGTGTTGGATGAGGCCACGGCAGCCGTGGACCTGGAAACGGACGACCTC 4597
Qy       1215 IleGlnLysLysIleArgGluLysPheAlaHisCysThrValLeuThrIleAlaHisArg 1234
Db       4598 ATCCAGTCCACCATCCGGACACAGTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGG 4657
Qy       1235 LeuAsnThrIleIleAspSerAspLysIleMetValLeuAspSerGlyArgLeuLysGlu 1254
Db       4658 CTCAACACCATCATGGACTACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAG 4717
Qy       1255 TyrAspGluProTyrValLeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGln 1274
Db       4718 TACGGCGCCCCATCGGACCTCCTGCAGCAGAGA---GGTCTTTTCTACAGCATGGCCAAA 4774
Qy       1275 GlnLeuGly---------LysAlaGluAlaAlaAlaLeuThrGluThrAlaLysGlnVal 1291
Db       4775 GACGCCGGCTTGGTGTGAGCCCCAGAGCTGGCATATCTGGTCAGAACTGCAGGGCCTATA 4834
Qy       1292 Tyr---------PheLysArgAsnTyrProHisIleGlyHisThrAspHisMetValThr 1308
Db       4835 TGCCAGCGCCCAGGGAGGAGTCAGTACCCCTG-GTAAACCAAGCCTCCCACACTGAAACC 4893
Qy       1309 AsnThrSerAsnGlyGlnProSerThrLeuThrIlePheGluThrAla 1324
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RESULT 9
US-11-045-578-3
; Sequence 3, Application US/11045578
; Publication No. US20060024685A1
; GENERAL INFORMATION:
; APPLICANT: HO, Rodney J.Y.
; APPLICANT: YANG, Ziping

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;  APPLICANT:  SHEN, Danny D.
;  APPLICANT:  WU, Daniel
;  TITLE OF INVENTION: NOVEL SEQUENCE VARIANTS OF MULTI-DRUG RESISTANCE GENES, MDR1 AND
;  TITLE OF INVENTION:  MRP1, AND RECOMBINANT CELLS EXPRESSING MRP1 AND MDR1 FOR
;  TITLE OF INVENTION:  ASSESSMENT OF DRUG PENETRATION AND DISPOSITION
;  FILE REFERENCE: 016336-002510US
;  CURRENT APPLICATION NUMBER: US/11/045,578
;  CURRENT FILING DATE:  2005-01-26
;  PRIOR APPLICATION NUMBER: US 60/539,362
;  PRIOR FILING DATE: 2004-01-26
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
;   LENGTH: 5011
;   TYPE: DNA
;   ORGANISM: human
US-11-045-578-3

Alignment Scores:
Pred. No.:              2.81e-209      Length:        5011
Score:                  2285.50        Matches:       528
Percent Similarity:     56.6%          Conservative:  274
Best Local Similarity:  37.3%          Mismatches:    491
Query Match:            33.7%          Indels:        124
DB:                     12             Gaps:          30

US-09-976-858-42 (1-1325) x US-11-045-578-3 (1-5011)

Qy          3 ProValTyrGlnGluVal------LysProAsnProLeuGlnAsp------AlaAsnLeu 18
              |||:::::: |||                ||||||||     :::      |||:::
Db        782 CCCCTGTTCTCGGAAACCATCCACGACCCTAATCCCTGCCCAGAGTCCAGCGCTTCCTTC 841

Qy         19 CysSerArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArg 38
                 ||||||:::  ||||||||:::       |||       |||:::::::::
Db        842 CTGTCGAGGATCACCTTCTGGTGGATCACAGGGTTGATTGTCCGGGGCTACCGCCAGCCC 901

Qy         39 LeuGluGluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGlu 58
              ||||||     |||::::::|||:::        ||||||   |||:::    :::
Db        902 CTGGAGGGCAGTGACCTCTGGTCCTTAAACAAGGAGGACACGTCGGAACAAGTCGTGCCT 961

Qy         59 GluLeuGlnGlyPheTrpAspLysGlu--------------------------------- 67
                 |||        |||  ||||||
Db        962 GTTTTGGTAAAGAACTGGAAGAAGGAATGCGCCAAGACTAGGAAGCAGCCGGTGAAGGTT 1021

Qy         68 ValLeuArgAlaGluAsnAspAlaGln--------------------------------- 76
              |||     :::::::::  ||||||
Db       1022 GTGTACTCCTCCAAGGATCCTGCCCAGCCGAAAGAGAGTTCCAAGGTGGATGCGAATGAG 1081

Qy         77 ------------------------------------------LysProSerLeuThrArg 82
                                                        |||||||||     :::
Db       1082 GAGGTGGAGGCTTTGATCGTCAAGTCCCCACAGAAGGAGTGGAACCCCTCTCTGTTTAAG 1141

Qy         83 AlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGlu 102
                 :::   |||    :::         :::|||:::         |||      |||
Db       1142 GTGTTATACAAGACCTTTGGGCCCTACTTCCTCATGAGCTTCTTCTTCAAGGCCATCCAC 1201

Qy        103 GluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsn 122
              :::                   |||      |||  |||:::::::       |||    |||
Db       1202 GACCTGATGATGTTTTCCGGGCCGCAGATCTTA---AAGTTGCTCATCAAGTTCGTGAAT 1258

Qy        123 TyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThr 142
                             |||:::   |||    :::              :::   ||||||||
Db       1259 ------------GACACGAAGGCCCCAGACTGGCAGGGCTACTTCTACACCGTGCTGCTG 1306

Qy        143 PheCysThrLeuIleLeu---AlaIleLeuHisHisLeuTyrPheTyrHisValGlnCys 161
              |||   |||        |||   ::::::   |||     ||||||:::
Db       1307 TTTGTCACTGCCTGCCTGCAGACCCTCGTGCTGCACCAGTACTTCCACATCTGCTTCGTC 1366

Qy        162 AlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeu 181
              :::||||||||||:::::::   |||:::         :::|||||||||||||||      :::
Db       1367 AGTGGCATGAGGATCAAGACCGCTGTCATTGGGGCTGTCTATCGGAAGGCCCTGGTGATC 1426

Qy        182 SerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAsp 201
              :::|||   |||         :::|||   |||:::||||||||||||:::|||   |||
Db       1427 ACCAATTCAGCCAGAAAATCCTCCACGGTCGGGGAGATTGTCAACCTCATGTCTGTGGAC 1486

Qy        202 ValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGln 221
                 :::|||    :::       :::::::::   :::|||:::   |||||||||
Db       1487 GCTCAGAGGTTCATGGACTTGGCCACGTACATTAACATGATCTGGTCAGCCCCCCTGCAA 1546

Qy        222 AlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMet 241
                 |||           ||||||||:::   :::|||   |||    |||||||||:::
Db       1547 GTCATCCTTGCTCTCTACCTCCTGTGGCTGAATCTGGGCCCTTCCGTCCTGGCTGGAGTG 1606

Qy        242 AlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeu 261
              ||||||::::::::::::::|||:::   :::                         :::
Db       1607 GCGGTGATGGTCCTCATGGTGCCCGTCAATGCTGTG--------------------ATG 1645

Qy        262 ArgSerLysThrAlaThrPhe---------------------ThrAspAlaArgIleArg 274
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Db       1646 GCGATGAAGACCAAGACGTATCAGGTGGCCCACATGAAGAGCAAAGACAATCGGATCAAG 1705

Qy        275 ThrMetAsnGluValIleThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSer 294
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Db       1706 CTGATGAACGAAATTCTCAATGGGATCAAAGTGCTAAAGCTTTATGCCTGGGAGCTGGCA 1765

Qy        295 PheSerAsnLeuIleThrAsnLeuArgLysLysGluIleSerLysIleLeuArgSerSer 314
              |||   :::   :::      :::||||||:::::::||   :::   :::|||:::
Db       1766 TTCAAGGACAAGGTGCTGGCCATCAGGCAGGAGGAGCTGAAGGTGCTGAAGAAGTCTGCC 1825

Qy        315 CysLeuArgGlyMetAsnLeuAlaSerPhePheSerAlaSerLysIleIleValPheVal 334
                 |||      :::         ::::::            ::::::
Db       1826 TACCTGTCAGCCGTGGGCACCTTCACCTGGGTCTGCACGCCCTTTCTGGTGGCCTTGTGC 1885

Qy        335 ThrPheThrThrTyrValLeuLeu------GlySerValIleThrAlaSerArgValPhe 352
              ||||||   ||||||   :::         :::::::::   |||         |||
Db       1886 ACATTTGCCGTCTACGTGACCATTGACGAGAACAACATCCTGGATGCCCAGACAGCCTTC 1945

Qy        353 ValAlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePheProSerAla 372
              |||::::::   |||:::      :::|||      :::   :::      |||
Db       1946 GTGTCTTTGGCCTTGTTCAACATCCTCCGGTTTCCCCTGAACATT---CTCCCCATGGTC 2002

Qy        373 IleGluArgValSerGluAlaIleValSerIleArgArgIleGlnThrPheLeuLeuLeu 392
              |||      :::   :::|||   ||||||::::::|||:::::::      ||||||
Db       2003 ATCAGCAGCATCGTGCAGGCGAGTGTCTCCCTCAAACGCCTGAGGATCTTTCTCTCCCAT 2062

Qy        393 AspGluIleSer------------GlnArgAsnArgGlnLeuProSerAspGlyLysLys 408
              :::|||:::               :::|||                  |||
Db       2063 GAGGAGCTGGAACCTGACAGCATCGAGCGACGGCCTGTCAAAGACGGCGGGGGCACGAAC 2122

Qy        409 MetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThrProThrLeu 428
                 :::   |||::::::   |||         |||   :::   |||:::   |||||||||
Db       2123 AGCATCACCGTGAGGAATGCCACATTCACCTGGGCCAGG---AGCGACCCTCCCACACTG 2179

Qy        429 GlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGlyProValGly 448
                 |||::::::|||::::::      |||   |||:::|||||||||||||   ||||||
Db       2180 AATGGCATCACCTTCTCCATCCCCGAAGGTGCTTTGGTGGCCGTGGTGGGCCAGGTGGGC 2239

Qy        449 AlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHisGlyLeu 468
              |||||||||||||||||||||||||:::|||   |||:::                |||
Db       2240 TGCGGAAAGTCGTCCCTGCTCTCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCAC 2299

Qy        469 ValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPheSerGlyThr 488
              |||::::::   |||   :::|||||||||   ||||||   |||:::   :::.   :::
Db       2300 GTGGCTATCAAGGGCTCCGTGGCCTATGTGCCACAGCAGGCCTGGATTCAGAATGATTCT 2359

Qy        489 LeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGluLysValIle 508
              ||||||   ||||||||||||||||   :::   |||:::      |||      ||||||
Db       2360 CTCCGAGAAAACATCCTTTTTGGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATA 2419

Qy        509 LysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThrValIle 528
              :::||||||||||||      ||||||:::::::|||      ||||||   |||   |||
Db       2420 CAGGCCTGTGCCCTCCTCCCAGACCTGGAAATCCTGCCCAGTGGGGATCGGACAGAGATT 2479

Qy        529 GlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAla 548
              |||::::::|||         ||||||||||||||||||   ||||||:::||||||||||
```

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Db   2480 GGCGAGAAGGGCGTGAACCTGTCTGGGGGCCAGAAGCAGCGCGTGAGCCTGGCCCGGGCC 2539
Qy    549 ValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGlu 568
Db   2540 GTGTACTCCAACGCTGACATTTACCTCTTCGATGATCCCCTCTCAGCAGTGGATGCCCAT 2599
Qy    569 ValSerArgHisLeuPheGluLeuCysIleCysGln------IleLeuHisGluLysIle 586
Db   2600 GTGGGAAAACACATCTTTGAAAATGTGATTGGCCCCAAGGGGATGCTGAAGAACAAGACG 2659
Qy    587 ThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIleLeu 606
Db   2660 CGGATCTTGGTCACGCACAGCATGAGCTACTTGCCGCAGGTGGACGTCATCATCGTCATG 2719
Qy    607 LysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIleAsp 626
Db   2720 AGTGGCGGCAAGATCTCTGAGATGGGCTCCTACCAGGAGCTGCTGGCTCGAGACGGCGCC 2779
Qy    627 PheGlySerLeuLeuLys-----------------------LysAspAsnGluGluSer 638
Db   2780 TTCGCTGAGTTCCTGCGTACCTATGCCAGCACAGAGCAGGAGCAGGATGCAGAGGAGAAC 2839
Qy    639 GluGlnProProValProGly------------ThrProThrLeuArgAsn--------- 651
Db   2840 GGGGTCACGGGCGTCAGCGGTCCAGGGAAGGAAGCAAAGCAAATGGAGAATGGCATGCTG 2899
Qy    652 ------------------------------ArgThrPheSerGluSerSerValTrpSer 661
Db   2900 GTGACGGACAGTGCAGGGAAGCAACTGCAGAGACAGCTCAGCAGCTCCTCCTCCTATAGT 2959
Qy    662 GlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsn 681
Db   2960 GGGGACATCAGCAGGCACCACAACAGCACCGCAGAACTGCAGAAAGCTGAGGCCAAGAAG 3019
Qy    682 ValProVal---ThrLeuSerGluGluAsnArgSerGlu---GlyLysValGlyPheGln 699
Db   3020 GAGGAGACCTGGAAGCTGATGGAGGCTGACAAGGCGCAGACAGGGCAGGTCAAGCTTTCC 3079
Qy    700 AlaTyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPhe------IlePheLeu 717
Db   3080 GTGTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTCCTTCCTCAGCATCTTCCTT 3139
Qy    718 IleLeuLeuAsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyr 737
Db   3140 TTCATGTGTAAC---------CATGTGTCCGCGCTGGCTTCCAACTATTGGCTCAGCCTC 3190
Qy    738 TrpAlaAsnLysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGlu 757
Db   3191 TGGACTGAT---------------GACCCCATCGTCAACGGGACTCAGGAGCACACGAAA 3235
Qy    758 ---LysLeuAspLeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrVal 776
Db   3236 GTCCGGCTGAGCGTCTATGGAGCCCTGGGCATTTCACAAGGGATCGCCGTG--------- 3286
Qy    777 LeuPheGlyIleAlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThr 796
Db   3287 ---TTTGGCTACTCCATGGCCGTGTCCATCGGGGGGATCTTG------GCTTCCCGCTGT 3337
Qy    797 LeuHisAsnLysMetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsn 816
Db   3338 CTGCACGTGGACCTGCTGCACAGCATCCTGCGGTCACCCATGAGCTTCTTTGAGCGGACC 3397
Qy    817 ProIleGlyArgIleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeu 836
Db   3398 CCCAGTGGGAACCTGGTGAACCGCTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATC 3457
Qy    837 ProLeuThrPheLeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerVal 856
Db   3458 CCGGAGGTCATCAAGATGTTCATGGGCTCCCTGTTCAACGTCATTGGTGCCTGCATCGTT 3517
Qy    857 AlaValAlaValIleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIle 876
Db   3518 ATCCTGCTGGCCACGCCCATCGCCGCCATCATCATCCCGCCCCTTGGCCTCATCTACTTC 3577
Qy    877 PheLeuArgArgTyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThr 896
Db   3578 TTCGTCCAGAGGTTCTACGTGGCTTCCTCCCGGCAGCTGAAGCGCCTCGAGTCGGTCAGC 3637
Qy    897 ArgSerProValPheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAla 916
Db   3638 CGCTCCCCGGTCTATTCCCATTTCAACGAGACCTTGCTGGGGGTCAGCGTCATTCGAGCC 3697
Qy    917 TyrLysAlaGluGluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGlu 936
Db   3698 TTCGAGGAGCAGGAGCGCTTCATCCACCAGAGTGACCTGAAGGTGGACGAGAACCAGAAG 3757
Qy    937 AlaTrpPheLeuPheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCys 956
Db   3758 GCCTATTACCCCAGCATCGTGGCCAACAGGTGGCTGGCCGTGCGGCTGGAGTGTGTGGGC 3817
Qy    957 AlaMetPheValIleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAla 976
Db   3818 AACTGCATCGTTCTGTTTGCTGCCCTGTTTGCGGTGATCTCCAGGCACAGCCTCAGTGCT 3877
Qy    977 GlyGlnValGlyLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCys 996
Db   3878 GGCTTGGTGGGCCTCTCAGTGTCTTACTCATTGCAGGTCACCACGTACTTGAACTGGCTG 3937
Qy    997 ValArgGlnSerAlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyr 1016
Db   3938 GTTCGGATGTCATCTGAAATGGAAACCAACATCGTGGCCGTGGAGAGGCTCAAGGAGTAT 3997
Qy   1017 ThrAspLeuGluLysGluAlaProTrpGluTyrGlnLys---ArgProProProAlaTrp 1035
Db   3998 TCAGAGACTGAGAAGGAGGCGCCCTGGCAAATCCAGGAGACAGCTCCGCCCAGCAGCTGG 4057
Qy   1036 ProHisGluGlyValIleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyPro 1055
Db   4058 CCCCAGGTGGGCCGAGTGGAATTCCGGAACTACTGCCTGCGCTACCGAGAGGACCTGGAC 4117
Qy   1056 LeuValLeuLysHisLeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGly 1075
Db   4118 TTCGTTCTCAGGCACATCAATGTCACGATCAATGGGGGAGAAAAGGTCGGCATCGTGGGG 4177
Qy   1076 ArgThrGlyAlaGlyLysSerSerLeuIleSerAlaLeuPheArgLeuSerGlu---Pro 1094
Db   4178 CGGACGGGAGCTGGGAAGTCGTCCCTGACCCTGGGCTTATTTCGGATCAACGAGTCTGCC 4237
Qy   1095 GluGlyLysIleTrpIleAspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArg 1114
Db   4238 GAAGGAGAGATCATCATCGATGGCATCAACATCGCCAAGATCGGCCTGCACGACCTCCGC 4297
Qy   1115 LysLysMetSerIleIleProGlnGluProValLeuPheThrGlyThrMetArgLysAsn 1134
Db   4298 TTCAAGATCACCATCATCCCCCAGGACCCTGTTTTGTTTTCGGGTTCCCTCCGAATGAAC 4357
Qy   1135 LeuAspProPheAsnGluHisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGln 1154
Db   4358 CTGGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGGCCCAC 4417
Qy   1155 LeuLysGluThrIleGluAspLeuProGlyLysMetAspThrGluLeuAlaGluSerGly 1174
Db   4418 CTGAAGGACTTCGTGTCAGCCCTTCCTGACAAGCTAGACCATGAATGTGCAGAAGGCGGG 4477
Qy   1175 SerAsnPheSerValGlyGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLys 1194
Db   4478 GAGAACCTCAGTGTCGGGCAGCGCCAGCTTGTGTGCCTAGCCCGGGCCCTGCTGAGGAAG 4537
Qy   1195 AsnGlnIleLeuIleIleAspGluAlaThrAlaAsnValAspProArgThrAspGluLeu 1214
Db   4538 ACGAAGATCCTTGTGTTGGATGAGGCCACGGCAGCCGTGGACCTGGAAACGGACGACCTC 4597
Qy   1215 IleGlnLysLysIleArgGluLysPheAlaHisCysThrValLeuThrIleAlaHisArg 1234
Db   4598 ATCCAGTCCACCATCCGGACACAGTTCGAGGACTGCACCGTCCTCACCATCGCCCACCGG 4657
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Qy       1235 LeuAsnThrIleIleAspSerAspLysIleMetValLeuAspSerGlyArgLeuLysGlu 1254
              ||||||||||||:::|||       :::::::::||||||||    |||   ::::::|||
Db       4658 CTCAACACCATCATGGACTACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAG 4717

Qy       1255 TyrAspGluProTyrValLeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGln 1274
              |||      |||      ||||||||    :::       ||||||||   |||    :::
Db       4718 TACGGCGCCCCATCGGACCTCCTGCAGCAGAGA---GGTCTTTTCTACAGCATGGCCAAA 4774

Qy       1275 GlnLeuGly---------LysAlaGluAlaAlaAlaLeuThrGluThrAlaLysGlnVal 1291
                    |||            |||   |||   |||      ||||||       :::
Db       4775 GACGCCGGCTTGGTGTGAGCCCCAGAGCTGGCATATCTGGTCAGAACTGCAGGGCCTATA 4834

Qy       1292 Tyr---------PheLysArgAsnTyrProHisIleGlyHisThrAspHisMetValThr 1308
                          :::      |||||   :::               |||       |||
Db       4835 TGCCAGCGCCCAGGGAGGAGTCAGTACCCCTG-GTAAACCAAGCCTCCCACACTGAAACC 4893

Qy       1309 AsnThrSerAsnGlyGlnProSerThrLeuThrIlePheGluThrAla 1324
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Db       4894 AAAACATAAAAACCAAACCCAGACAACCAAAACATATTCAAAGCAGCA 4941
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RESULT 10
US-11-045-578-2
; Sequence 2, Application US/11045578
; Publication No. US20060024685A1
; GENERAL INFORMATION:
; APPLICANT: HO, Rodney J.Y.
; APPLICANT: YANG, Ziping
; APPLICANT: SHEN, Danny D.
; APPLICANT: WU, Daniel
; TITLE OF INVENTION: NOVEL SEQUENCE VARIANTS OF MULTI-DRUG RESISTANCE GENES, MDR1 AND
; TITLE OF INVENTION: MRP1, AND RECOMBINANT CELLS EXPRESSING MRP1 AND MDR1 FOR
; TITLE OF INVENTION: ASSESSMENT OF DRUG PENETRATION AND DISPOSITION
; FILE REFERENCE: 016336-002510US
; CURRENT APPLICATION NUMBER: US/11/045,578
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US 60/539,362
; PRIOR FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 4587
; TYPE: DNA
; ORGANISM: mouse
US-11-045-578-2

Alignment Scores:

Pred. No.:	3.7e-207	Length:	4587
Score:	2263.00	Matches:	491
Percent Similarity:	57.3%	Conservative:	288
Best Local Similarity:	36.1%	Mismatches:	468
Query Match:	33.3%	Indels:	112
DB:	12	Gaps:	23

US-09-976-858-42 (1-1325) x US-11-045-578-2 (1-4587)

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Qy          3 ProValTyrGlnGluVal-----------LysProAsnProLeuGlnAspAlaAsnLeu 18
              |||::::::  |||                         |||   |||     |||:::
Db        586 CCCCTGTTCTCTGAAACTGTCCATGACCGGAATCCATGCCCAGAATCCAGTGCCTCTTTC 645

Qy         19 CysSerArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArg 38
                 ||||||:::   |||||||||:::            :::      |||:::::::::
Db        646 CTTTCCAGGATTACTTTCTGGTGGATTACAGGGATGATGGTGCACGGCTACCGCCAGCCC 705

Qy         39 LeuGluGluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGlu 58
              ||||||       |||::::::|||:::      ||||||   |||:::      :::
Db        706 CTGGAGAGCAGTGACCTCTGGTCATTGAATAAGGAGGACACATCAGAAGAAGTGGTACCT 765

Qy         59 GluLeuGlnGlyPheTrpAspLysGlu--------------------------------- 67
                 |||         |||   ||||||
Db        766 GTGCTGGTGAATAACTGGAAGAAGGAATGTGATAAGTCAAGGAAGCAGCCTGTACGGATT 825

Qy         67 ------------------------------------------------------------ 67

Db        826 GTGTATGCCCCTCCCAAAGATCCCAGCAAGCCTAAGGGAAGTTCCCAGTTGGATGTGAAT 885

Qy         68 -----------------ValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThr 81
                               ::::::::::::   :::      ::::::|||||||||
Db        886 GAGGAGGTGGAGGCACTGATTGTCAAGTCACCCCACAAGGATCGGGAGCCCTCTCTGTTC 945

Qy         82 ArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIle 101
              :::   :::   |||   :::      :::|||:::      ::::::         :::
Db        946 AAGGTGTTATACAAGACTTTTGGTCCCTACTTCCTCATGAGCTTCCTGTACAAGGCCCTT 1005

Qy        102 GluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGlu 121
                 :::                  |||      |||      |||||||||:::
Db       1006 CATGACCTGATGATGTTTGCCGGCCCCAAGATCTTGGAATTGATTATCAACTTCGTGAAT 1065

Qy        122 AsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeu 141
              :::   :::   |||                        |||   |||      :::|||
Db       1066 GACAGGGAGGCTCCCGACTGG-----------CAGGGCTACTTTTACACAGCACTGCTG 1113

Qy        142 ThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCys 161
                             :::      :::         |||   ||||||:::
Db       1114 TTTGTCAGCGCCTGTCTGCAGACACTGGCACTCCACCAGTACTTTCATATCTGCTTCGTC 1173

Qy        162 AlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeu 181
              :::|||||||||::::::      |||:::         :::|||||||||||||   :::
Db       1174 AGTGGCATGCGCATCAAGACTGCTGTGGTGGGCGCTGTCTATCGTAAGGCTCTTTTGATC 1233

Qy        182 SerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAsp 201
              :::|||   |||         :::|||   |||:::||||||||||||:::|||   |||
Db       1234 ACCAATGCAGCTAGAAAATCTTCCACGGTCGGAGAGATTGTCAACCTCATGTCCGTGGAT 1293

Qy        202 ValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGln 221
                 :::|||      :::      :::::::::   :::|||:::   |||||||||
Db       1294 GCTCAGCGCTTCATGGACTTGGCCACGTACATTAACATGATCTGGTCAGCCCCTCTGCAA 1353

Qy        222 AlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMet 241
                 |||               ||||||:::   :::|||   |||   |||||||||:::
Db       1354 GTCATCCTAGCCCTCTACTTCCTGTGGCTGAGCCTGGGCCCTTCTGTGCTGGCTGGAGTG 1413

Qy        242 AlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeu 261
              ||||||:::|||:::::::::||||||   :::                        :::
Db       1414 GCTGTGATGATTCTCATGGTACCCTTAAATGCTGTG---------------------ATG 1452

Qy        262 ArgSerLysThrAlaThrPhe---------------------ThrAspAlaArgIleArg 274
                    ||||||   |||:::                      |||   ||||||:::
Db       1453 GCCATGAAGACCAAGACCTACCAGGTGGCACACATGAAGAGCAAAGACAACCGAATCAAG 1512

Qy        275 ThrMetAsnGluValIleThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSer 294
                 |||||||||::::::   ||||||::::::::|||:::||||||||||||   :::
Db       1513 CTGATGAACGAGATCCTCAATGGGATCAAAGTCCTCAAGCTGTACGCCTGGGAGCTGGCC 1572

Qy        295 PheSerAsnLeuIleThrAsnLeuArgLysLysGluIleSerLysIleLeuArgSerSer 314
              |||   :::   :::   ::::::|||::::::|||:::         :::   :::|||:::
Db       1573 TTCCAGGACAAAGTCATGAGCATCAGGCAGGAGGAGCTCAAGGTGCTGAAGAAATCTGCC 1632

Qy        315 CysLeuArgGlyMetAsnLeuAlaSerPhePheSerAlaSerLysIleIleValPheVal 334
                 |||      :::         ::::::            ::::::
Db       1633 TACCTGGCAGCTGTAGGCACATTCACGTGGGTGTGCACACCTTTCCTGGTGGCCCTGTCA 1692

Qy        335 ThrPheThrThrTyrValLeuLeuGly------SerValIleThrAlaSerArgValPhe 352
              ||||||      :::|||   :::         :::::::::   |||   :::   |||
Db       1693 ACCTTTGCTGTCTTTGTGACTGTGGATGAGAGAAATATCCTAGATGCAAAGAAAGCCTTT 1752

Qy        353 ValAlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePheProSerAla 372
              |||::::::   |||:::      :::|||      :::   :::         |||
Db       1753 GTGTCCCTAGCCCTGTTCAATATCTTGCGCTTCCCACTCAACATC---CTGCCCATGGTT 1809

Qy        373 IleGluArgValSerGluAlaIleValSerIleArgArgIleGlnThrPheLeuLeuLeu 392
              |||      :::   :::|||   ||||||:::::::|||::::::      ||||||
Db       1810 ATCAGCAGCATTGTGCAGGCCAGCGTGTCCCTCAAGCGTCTCAGGATTTTTCTGTCTCAT 1869.

Qy        393 AspGluIle---------SerGlnArgAsnArgGlnLeuProSerAspGlyLysLysMet 409
              :::|||:::          |||         |||   :::   |||
Db       1870 GAGGAGCTGGAGCCAGACAGCATTGAGCGGAGGTCGATCAAGAGTGGAGAAGGGAATAGC 1929
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Qy        410 ValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThrProThrLeuGln 429
Db       1930 ATCACTGTGAAGAATGCAACCTTCACTTGGGCCAGG---GGTGAACCTCCCACACTGAAT 1986

Qy        430 GlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGlyProValGlyAla 449
Db       1987 GGCATCACCTTCTCCATTCCTGAAGGAGCCCTTGTGGCCGTGGTGGGCCAGGTAGGCTGC 2046

Qy        450 GlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHisGlyLeuVal 469
Db       2047 GGGAAGTCATCTCTGCTGTCAGCCCTGCTGGCTGAGATGGACAAGGTGGAGGGACATGTG 2106

Qy        470 SerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPheSerGlyThrLeu 489
Db       2107 ACTCTCAAGGGCTCCGTGGCCTACGTGCCCCAGCAGGCCTGGATTCAGAATGACTCTCTC 2166

Qy        490 ArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGluLysValIleLys 509
Db       2167 CGAGAGAACATACTGTTTGGGCACCCCCTGCAGGAAAATTACTACAAGGCAGTTATGGAA 2226

Qy        510 AlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThrValIleGly 529
Db       2227 GCCTGTGCCCTTCTTCCAGATTTGGAAATCCTGCCCAGTGGGGACCGCACAGAGATCGGT 2286

Qy        530 AspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAlaVal 549
Db       2287 GAGAAGGGTGTGAACCTGTCAGGGGGCCAGAAGCAGCGTGTGAGCCTGGCCCGGGCTGTG 2346

Qy        550 TyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGluVal 569
Db       2347 TACTCTAACTCTGACATCTACCTCTTTGATGACCCCCTCTCGGCTGTGGATGCACATGTT 2406

Qy        570 SerArgHisLeuPheGluLeuCysIle------CysGlnIleLeuHisGluLysIleThr 587
Db       2407 GGGAAGCACATCTTTGAGAAGGTGGTTGGTCCCATGGGCCTACTGAAGAACAAGACACGG 2466

Qy        588 IleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIleLeuLys 607
Db       2467 ATCCTGGTCACCCATGGTATCAGCTACCTGCCCCAAGTGGATGTCATCATTGTCATGAGT 2526

Qy        608 AspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIleAspPhe 627
Db       2527 GGCGGCAAGATCTCAGAGATGGGTTCTTATCAGGAGCTGCTAGACCGGGATGGGGCCTTC 2586

Qy        628 GlySerLeuLeuLys--------------------------------LysAspAsnGlu 636
Db       2587 GCTGAGTTCCTGCGCACCTATGCCAACGCTGAGCAGGACCTGGCCTCGGAGGATGACAGT 2646

Qy        637 GluSer------------GluGlnProProValProGly------------ThrProThr 648
Db       2647 GTCAGTGGTTCAGGGAAGGAGTCAAAGCCGGTGGAAAATGGGATGCTGGTGACAGACACC 2706

Qy        649 Leu---------ArgAsnArgThrPheSerGluSerSerValTrpSerGlnGlnSerSer 665
Db       2707 GTAGGAAAGCACCTGCAGAGGCATCTCAGCAACTCGTCTTCCCACAGTGGGGATACCAGC 2766

Qy        666 ArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnValProValThr 685
Db       2767 CAGCAACACAGCAGCATAGCCGAACTGCAGAAGGCTGGAGCTAAGGAGGAGACGTGGAAG 2826

Qy        686 LeuSerGluGluAsnArgSerGlu---GlyLysValGlyPheGlnAlaTyrLysAsnTyr 704
Db       2827 CTAATGGAAGCAGACAAGGCCCAGACAGGGCAGGTGCAGCTGTCAGTGTACTGGAACTAC 2886

Qy        705 PheArgAlaGlyAlaHisTrpIleValPhe------IlePheLeuIleLeuLeuAsnThr 722
Db       2887 ATGAAGGCCATTGGCCTCTTCATCACCTTCTTGAGTATCTTCCTTTTCCTGTGCAAC--- 2943

Qy        723 AlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGln 742
Db       2944 ------CATGTATCTGCACTGGCCTCTAACTATTGGCTGAGCCTCTGGACAGATGACCCC 2997

Qy        743 SerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsn 762
Db       2998 CCTGTTGTCAATGGGACT--------------------------CAGGCGAACAGGAAT 3030

Qy        763 TrpTyrLeuGlyIleTyrSer------GlyLeuThrValAlaThrValLeuPheGlyIle 780
Db       3031 TTTCGGCTGAGTGTCTATGGGGCCTTGGGCATCTTGCAAGGTGCAGCAATATTTGGCTAC 3090

Qy        781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
Db       3091 TCCATGGCTGTGTCCATCGGGGGCATCTTT------GCCTCCCGTCGCTTGCACCTGGAC 3144

Qy        801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820
Db       3145 CTGCTATACAATGTTCTTCGATCACCCATGAGTTTCTTCGAGCGTACACCCAGTGGGAAC 3204

Qy        821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
Db       3205 CTAGTGAACCGATTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCGCAGGTCATC 3264

Qy        841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860
Db       3265 AAGATGTTCATGGGTTCACTCTTCAGTGTCATTGGAGCTGTCATCATCATCCTACTGGCC 3324

Qy        861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
Db       3325 ACGCCCATTGCCGCAGTCATCATCCCACCCTTGGGTCTGGTTTACTTCTTTGTGCAGAGG 3384

Qy        881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900
Db       3385 TTCTATGTGGCTTCCTCAAGACAACTGAAGCGCCTGGAGTCTGTCAGCCGTTCCCCTGTG 3444

Qy        901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
Db       3445 TACTCACACTTCAATGAGACCTTGCTGGGAGTCAGTGTCATCCGTGCTTTTGAGGAGCAG 3504

Qy        921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
Db       3505 GAGCGCTTCATTCACCAGAGTGACCTGAAAGTAGATGAGAACCAGAAGGCCTACTACCCC 3564

Qy        941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
Db       3565 AGCATTGTGGCCAACAGATGGCTTGCTGTGCGCCTTGAGTGTGTGGGCAACTGCATTGTG 3624

Qy        961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
Db       3625 CTGTTTGCTGCCCTCTTTGCAGTCATCTCCCGGCACAGCCTCAGTGCTGGCTTGGTGGGC 3684

Qy        981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
Db       3685 CTCTCTGTGTCTTACTCACTGCAGATAACTGCATACTTGAACTGGCTGGTTCGAATGTCC 3744

Qy       1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
Db       3745 TCGGAGATGGAGACCAACATTGTGGCAGTGGAGAGACTGAAGGAGTATTCTGAAACAGAG 3804

Qy       1021 LysGluAlaProTrpGluTyrGlnLysArgProProProAla---TrpProHisGluGly 1039
Db       3805 AAGGAGGCTCCTTGGCAAATCCAGGAAACAGCTCCACCCAGCACCTGGCCCCATTCAGGC 3864

Qy       1040 ValIleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLys 1059
Db       3865 CGTGTAGAGTTCCGGGATTACTGCCTGAGGTATCGAGAAGACTTGGACTTGGTTCTCAAG 3924

Qy       1060 HisLeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAla 1079
Db       3925 CACATAAATGTCACCATTGAGGGTGGAGAAAAGGTGGGTATTGTAGGTCGTACGGGAGCT 3984

Qy       1080 GlyLysSerSerLeuIleSerAlaLeuPheArgLeuSerGlu---ProGluGlyLysIle 1098
Db       3985 GGGAAATCATCTCTCACCCTGGGTTTGTTCCGGATCAATGAGTCTGCAGAAGGGGAGATC 4044

Qy       1099 TrpIleAspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSer 1118
```

```
Db       4045 ATCATTGATGGGGTCAACATCGCCAAGATCGGCCTGCACAACCTGCGCTTCAAGATCACC 4104

Qy       1119 IleIleProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPhe 1138
Db       4105 ATCATTCCACAGGATCCTGTTTTGTTCTCGGGTTCCCTCCGCATGAACTTGGACCCTTTC 4164

Qy       1139 AsnGluHisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThr 1158
Db       4165 AGTCAGTATTCTGATGAAGAAGTCTGGATGGCCCTGGAGCTTGCTCACCTAAAGGGCTTT 4224

Qy       1159 IleGluAspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSer 1178
Db       4225 GTGTCAGCCTTGCCTGACAAGCTGAACCATGAGTGTGCAGAAGGTGGAGAGAACCTGAGT 4284

Qy       1179 ValGlyGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeu 1198
Db       4285 GTGGGGCAGCGACAGCTTGTGTGCCTGGCCCGGGCTCTGCTGAGGAAGACAAAGATTCTA 4344

Qy       1199 IleIleAspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLys 1218
Db       4345 GTGTTGGACGAGGCTACCGCAGCTGTGGACCTAGAGACAGATAACCTTATCCAGTCCACC 4404

Qy       1219 IleArgGluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIle 1238
Db       4405 ATCCGGACGCAGTTTGAAGACTGTACTGTGCTCACGATTGCTCATCGGCTTAACACCATA 4464

Qy       1239 IleAspSerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluPro 1258
Db       4465 ATGGACTACACACGGGTTATTGTCCTGGACAAAGGAGAAGTTCGGGAGTGTGGTGCACCC 4524

Qy       1259 TyrValLeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGly 1277
Db       4525 TCTGAGCTCCTGCAGCAAAGA---GGCATCTTCTACAGCATGGCCAAGGATGCTGGC 4578
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RESULT 11
US-11-045-578-1
; Sequence 1, Application US/11045578
; Publication No. US20060024685A1
; GENERAL INFORMATION:
; APPLICANT: HO, Rodney J.Y.
; APPLICANT: YANG, Ziping
; APPLICANT: SHEN, Danny D.
; APPLICANT: WU, Daniel
; TITLE OF INVENTION: NOVEL SEQUENCE VARIANTS OF MULTI-DRUG RESISTANCE GENES, MDR1 AND
; TITLE OF INVENTION: MRP1, AND RECOMBINANT CELLS EXPRESSING MRP1 AND MDR1 FOR
; TITLE OF INVENTION: ASSESSMENT OF DRUG PENETRATION AND DISPOSITION
; FILE REFERENCE: 016336-002510US
; CURRENT APPLICATION NUMBER: US/11/045,578
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US 60/539,362
; PRIOR FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 4599
;   TYPE: DNA
;   ORGANISM: rat
US-11-045-578-1

Alignment Scores:

Pred. No.:	1.87e-204	Length:	4599
Score:	2235.00	Matches:	493
Percent Similarity:	57.2%	Conservative:	288
Best Local Similarity:	36.1%	Mismatches:	463
Query Match:	32.9%	Indels:	122
DB:	12	Gaps:	26

US-09-976-858-42 (1-1325) x US-11-045-578-1 (1-4599)

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Qy          3 ProValTyrGlnGluVal------LysProAsnProLeuGlnAsp------AlaAsnLeu 18
Db        586 CCCTTGTTCTCTGAAACTGTCCGTGACCCGAATCCATGTCCAGAATCGAGTGCCTCTTTT 645

Qy         19 CysSerArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArg 38
Db        646 CTTTCCAGGATCACTTTTGGTGGATTACAGGGATGATGGTGCAGGGCTACCGCCAGCCC 705

Qy         39 LeuGluGluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGlu 58
Db        706 CTGAAGAGCAGTGACCTCTGGTCATTGAATAAAGAGGACACGTCAGAAGAAGTGGTACCT 765

Qy         59 GluLeuGlnGlyPheTrpAspLysGlu------------------------------- 67
Db        766 GTGCTGGTGAATAACTGGAAGAAGGAATGTGTTAAGTCGAGGAAGCAGCCTGTACGGATT 825

Qy         67 ------------------------------------------------------------ 67
Db        826 GTGTATGCCCCTCCCAAAGATCCCACCAAGCCTAAGGGAAGTTCTCAGTTGGATGTGAAT 885

Qy         68 ------------------ValLeuArgAlaGluAsnAspAlaGlnLysProSerLeuThr 81
Db        886 GAGGAAGTGGAGGCACTGATTGTCAAGTCATCCCACAAGGACCGGGACCCCTCTCTGTTC 945

Qy         82 ArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIle 101
Db        946 AAGGTGTTGTACAAGACCTTTGGGCCCTACTTCCTCATGAGCTTCCTGTACAAGGCCCTT 1005

Qy        102 GluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGlu 121
Db       1006 CATGACCTGATGATGTTTGCTGGCCCTGAGATCTTGGAATTGATTATCAACTTCGTGAAT 1065

Qy        122 AsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeu 141
Db       1066 GACAGGGAGGCCCCTGACTGG------------CAGGGCTACTTGTACACAGCACTGCTG 1113

Qy        142 ThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCys 161
Db       1114 TTTGTCAGTGCCTGTCTGCAGACACTGGCACTCCACCAGTACTTTCATATCTGCTTCGTC 1173

Qy        162 AlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeu 181
Db       1174 ACCGGCATGCGCATCAAGACTGCTGTGGTGGGCGCTGTTTACCGCAAGGCTCTTGTGATC 1233

Qy        182 SerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAsp 201
Db       1234 ACCAATTCAGCTAGAAAATCGTCCACAGTTGGAGAGATTGTCAACCTCATGTCCGTGGAT 1293

Qy        202 ValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGln 221
Db       1294 GCCCAGCGCTTCATGGACTTGGCCACGTATATTAACATGATCTGGTCAGCCCCTCTGCAA 1353

Qy        222 AlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMet 241
Db       1354 GTCACCCTAGCCCTCTACTTCCTGTGGCTGAACCTGGGCCCTTCTGTGCTGGCTGGGGTG 1413

Qy        242 AlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeu 261
Db       1414 GCTGTTATGATCCTCATGGTGCCCTTCAATGCTGTG---------------------ATG 1452

Qy        262 ArgSerLysThrAlaThrPhe---------------------ThrAspAlaArgIleArg 274
Db       1453 GCCATGAAGACCAAGACTTACCAGGTGGCACACATGAAGAGCAAAGACAACCGAATCAAG 1512

Qy        275 ThrMetAsnGluValIleThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSer 294
Db       1513 CTGATGAACGAGATCCTCAATGGGATCAAAGTACTCAAATTGTACGCCTGGGAGCTGGCT 1572

Qy        295 PheSerAsnLeuIleThrAsnLeuArgLysLysGluIleSerLysIleLeuArgSerSer 314
Db       1573 TTCCAGGACAAAGTTATGAACATCAGGCAGGAGGAGCTGAAGGTGCTGAAGAAATCCGCC 1632

Qy        315 CysLeuArgGlyMetAsnLeuAlaSerPhePheSerAlaSerLysIleIleValPheVal 334
Db       1633 TACCTGGCGGCTGTGGGCACATTCACATGGGTTTGCACACCTTTCCTGGTGGCTCTGTCA 1692
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Qy     335 ThrPheThrThrTyrValLeuLeuGly------SerValIleThrAlaSerArgValPhe 352
Db    1693 ACCTTTGCTGTCTTTGTGACTGTGGACGAGAAGAACATCCTAGATGCAAAGAAAGCCTTT 1752

Qy     353 ValAlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePheProSerAla 372
Db    1753 GTATCCCTAGCCCTGTTCAATATCTTGCGCTTCCCACTCAACATC---CTACCCATGGTC 1809

Qy     373 IleGluArgValSerGluAlaIleValSerIleArgArgIleGlnThrPheLeuLeuLeu 392
Db    1810 ATCAGCAGCATTGTGCAGGCCAGCGTGTCCCTCAAGCGTCTCAGGATCTTTCTGTCTCAC 1869

Qy     393 AspGluIleSer------------GlnArgAsnArgGlnLeuProSerAspGlyLysLys 408
Db    1870 GAGGAGCTGGAGCCAGACAGCATCGAGCGATGGTCGATCAAGGATGGTGGAGGGATGAAT 1929

Qy     409 MetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThrProThrLeu 428
Db    1930 AGCATCACTGTGAAGAATGCAACCTTCACTTGGGCCAGG---GATGAACCTCCCACACTG 1986

Qy     429 GlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValValGlyProValGly 448
Db    1987 AATGGCATCACCTTCGCCATCCCTGATGGAGCCCTTGTGGCCGTGGTGGGCCAGGTAGGC 2046

Qy     449 AlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHisGlyLeu 468
Db    2047 TGTGGGAAGTCATCTCTGCTGTCAGCCCTGCTGGCTGAGATGGACAAAGTGGAGGGACAT 2106

Qy     469 ValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPheSerGlyThr 488
Db    2107 GTGACTCTCAAGGGCTCCGTGGCCTATGTGCCCCAGCAGGCCTGGATTCAGAATGACTCT 2166

Qy     489 LeuArgSerAsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGluLysValIle 508
Db    2167 CTCCGAGAGAACATACTGTTTGGGCGCCCCCTGCAGGAACATTGCTACAAGGCGGTGATG 2226

Qy     509 LysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThrValIle 528
Db    2227 GAGGCCTGTGCCCTCCTTCCGGATTTGGAAATCCTTCCCAGTGGGGACCTCACAGAGATT 2286

Qy     529 GlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAla 548
Db    2287 GGTGAGAAGGGTGTGAACCTGTCGGGGGGCCAGAAGCAGCGTGTGAGCCTGGCTCGGGCT 2346

Qy     549 ValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGlu 568
Db    2347 GTGTATTGTAACTCTGACATCTACCTCTTGGACGACCCCCTCTCGGCTGTGGATGCACAT 2406

Qy     569 ValSerArgHisLeuPheGluLeuCysIle------CysGlnIleLeuHisGluLysIle 586
Db    2407 GTTGGGAAGCACATCTTTGAGAAGGTGGTGGGTCCCATGGGCCTACTGAAGAACAAGACA 2466

Qy     587 ThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIleLeu 606
Db    2467 CGGATCCTGGTCACCCATGGTATCAGCTACCTGCCCCAAGTGGATGTCATCATTGTCATG 2526

Qy     607 LysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIleAsp 626
Db    2527 AGTGGCGGCAAGATCTCAGAGATGGGATCTTATCAGGAGCTGCTAGACCGGGATGGGGCC 2586

Qy     627 PheGly--------------------------------SerLeuLeuLysLysAspAsn 635
Db    2587 TTTGCTGAGTTCGTGCGCACCTATGCCAACACTGAGCAGGACCTGGCTTCAGAGGATGAC 2646

Qy     636 GluGluSer---------------------GluGlnProProValPro------------ 644
Db    2647 AGTAAGAATGGTGTCAGTGGTTTAGGGAAGGAGTCAAAGCCGGTGGAAAATGGGATACTG 2706

Qy     645 ---------------GlyThrProThrLeuArg------AsnArgThrPheSerGluSer 657
Db    2707 GTGACAGACGCAGTAGGGAAGCCCCTGCAGAGGCATCTCAGCAACTCTTCTTCCCACAGT 2766

Qy     658 SerValTrpSerGlnGln---SerSerArgProSerLeuLysAspGlyAlaLeuGluSer 676
Db    2767 GTGGTTACTAACCAGCAGCACAGCAGCACAGCCGAGCTGCAGAAGTCTGGGGTTAAGGAG 2826

Qy     677 GlnAspThrGluAsnValProValThrLeuSerGluGluAsnArgSerGlu---GlyLys 695
Db    2827 GAGACTTGGAAG---------------CTGATGGAAGCAGACAAGGCCCAGACAGGGCAG 2871

Qy     696 ValGlyPheGlnAlaTyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPhe--- 714
Db    2872 GTGAAGCTTTCCGTGTACTGGAACTACATGAAGGCCATTGGCCTCTGCATCTCCTTCTTG 2931

Qy     715 ---IlePheLeuIleLeuLeuAsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrp 733
Db    2932 AGTATCTTCCTTTTCCTGTGCAAT---------CATGTATCTGCACTGGCTTCTAACTAT 2982

Qy     734 TrpLeuSerTyrTrpAlaAsnLysGlnSerMetLeuAsnValThrValAsnGlyGlyGly 753
Db    2983 TGGCTGAGTCTCTGGACAGATGACCGCCCTGCTGTCAATGGGACTCAGGAG--------- 3033

Qy     754 AsnValThrGluLysLeuAspLeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrVal 773
Db    3034 AACAGGAATTTTCGACTAAGTGTCTATGGGGCCTTGGGCATCTTGCAAGGTGTGGCAGTA 3093

Qy     774 AlaThrValLeuPheGlyIleAlaArgSerLeuLeuValPheTyrValLeuValAsnSer 793
Db    3094 ------------TTTGGCTATTCCATGGCTGTGTCCATTGGGGGCATCTTT------GCC 3135

Qy     794 SerGlnThrLeuHisAsnLysMetPheGluSerIleLeuLysAlaProValLeuPhePhe 813
Db    3136 TCCCGTCGCCTGCACCTAGACCTGCTACAGAATGTCCTGCGATCACCCATGAGTTTCTTT 3195

Qy     814 AspArgAsnProIleGlyArgIleLeuAsnArgPheSerLysAspIleGlyHisLeuAsp 833
Db    3196 GAGCGTACACCCAGTGGGAACCTAGTGAACCGATTCTCCAAGGAGTTGGACACAGTGGAC 3255

Qy     834 AspLeuLeuProLeuThrPheLeuAspPheIleGlnThrLeuLeuGlnValValGlyVal 853
Db    3256 TCCATGATCCCGCAGGTCATCAAGATGTTCATGGGTTCACTCTTCAGTGTCATTGGAGCT 3315

Qy     854 ValSerValAlaValAlaValIleProTrpIleAlaIleProLeuValProLeuGlyIle 873
Db    3316 GTCATCATCATCCTACTGGCTACGCCCATTGCCGCAGTCATCATCCCACCCTTGGGTCTG 3375

Qy     874 IlePheIlePheLeuArgArgTyrPheLeuGluThrSerArgAspValLysArgLeuGlu 893
Db    3376 GTTTACTTCTTTGTGCAGAGGTTCTATGTGGCCTCCTCTCGACAGCTGAAGCGCCTGGAG 3435

Qy     894 SerThrThrArgSerProValPheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThr 913
Db    3436 TCTGTCAGTCGTTCCCCTGTGTACTCACACTTCAATGAGACCTTGCTGGGGGTCAGTGTC 3495

Qy     914 IleArgAlaTyrLysAlaGluGluArgCysGlnGluLeuPheAspAlaHisGlnAspLeu 933
Db    3496 ATCCGTGCCTTTGAGGAACAGGAGCGCTTCATTCGCCAAAGTGACCTGAAAGTAGATGAG 3555

Qy     934 HisSerGluAlaTrpPheLeuPheLeuThrThrSerArgTrpPheAlaValArgLeuAsp 953
Db    3556 AACCAGAAGGCCTACTACCCCAGCATTGTGGCCAACAGGTGGCTTGCTGTGCGCCTGGAG 3615

Qy     954 AlaIleCysAlaMetPheValIleIleValAlaPheGlySerLeuIleLeuAlaLysThr 973
Db    3616 TGTGTGGGCAACTGCATTGTGCTGTTTGCTGCCCTTTTCGCAGTCATCTCCCGGCATAGC 3675

Qy     974 LeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPhe 993
Db    3676 CTCAGTGCTGGCTTGGTGGGTCTCTCTGTGTCTTACTCACTGCAGATAACTGCATACTTG 3735

Qy     994 GlnTrpCysValArgGlnSerAlaGluValGluAsnMetMetIleSerValGluArgVal 1013
Db    3736 AACTGGCTAGTTCGAATGTCCTCTGAGATGGAGACCAACATTGTGGCAGTGGAGAGACTG 3795

Qy    1014 IleGluTyrThrAspLeuGluLysGluAlaProTrpGluTyrGlnLysArgProProPro 1033
```

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Db       3796 AAGGAATATTCTGAAACGGAGAAGGAGGCTTCTTGGCAAATCCAAGAGACAGCTCCACCC 3855

Qy       1034 Ala---TrpProHisGluGlyValIleIlePheAspAsnValAsnPheMetTyrSerPro 1052

Db       3856 AGCACCTGGCCCCATTCAGGCCGTGTAGAGTTCCGGGATTACTGCTTGAGGTATCGAGAA 3915

Qy       1053 GlyGlyProLeuValLeuLysHisLeuThrAlaLeuIleLysSerGlnGluLysValGly 1072

Db       3916 GACTTGGACTTGGTTCTCAAGCACATAAATGTCACCATTGAGGGTGGAGAAAAGGTTGGT 3975

Qy       1073 IleValGlyArgThrGlyAlaGlyLysSerSerLeuIleSerAlaLeuPheArgLeuSer 1092

Db       3976 ATTGTGGGTCGTACAGGAGCTGGGAAATCATCTCTCACCCTGGGTTTGTTCCGGATCAAT 4035

Qy       1093 Glu---ProGluGlyLysIleTrpIleAspLysIleLeuThrThrGluIleGlyLeuHis 1111

Db       4036 GAGTCTGCAGAAGGGGAGATCATCATTGATGGGATAAACATTGCTAAGATTGGCCTGCAC 4095

Qy       1112 AspLeuArgLysLysMetSerIleIleProGlnGluProValLeuPheThrGlyThrMet 1131

Db       4096 AACCTGCGCTTCAAGATCACCATCATTCCACAGGATCCTGTTTTGTTCCCGGGTTCCCTC 4155

Qy       1132 ArgLysAsnLeuAspProPheAsnGluHisThrAspGluGluLeuTrpAsnAlaLeuGln 1151

Db       4156 CGCATGAACCTGGACCCTTTCAGTCAGTATTCTGATGAAGAAGTCTGGATGGCTCTGGAG 4215

Qy       1152 GluValGlnLeuLysGluThrIleGluAspLeuProGlyLysMetAspThrGluLeuAla 1171

Db       4216 CTTGCTCACCTGAAGGGCTTTGTGTCAGCCTTGCCTGACAAGCTGAACCATGAGTGTGCA 4275

Qy       1172 GluSerGlySerAsnPheSerValGlyGlnArgGlnLeuValCysLeuAlaArgAlaIle 1191

Db       4276 GAAGGTGGAGAGAATCTGAGTGTGGGGCAGCGACAGCTTGTGTGCCTGGCCCGGGCTTTG 4335

Qy       1192 LeuArgLysAsnGlnIleLeuIleIleAspGluAlaThrAlaAsnValAspProArgThr 1211

Db       4336 CTGAGGAAGACAAAGATTCTAGTGTTGGACGAGGCTACAGCAGCTGTGGATCTGGAGACA 4395

Qy       1212 AspGluLeuIleGlnLysLysIleArgGluLysPheAlaHisCysThrValLeuThrIle 1231

Db       4396 GATGACCTTATTCAGTCCACCGTCCGGACGCAGTTTGAAGACAGTACTGTGCTCACTATT 4455

Qy       1232 AlaHisArgLeuAsnThrIleIleAspSerAspLysIleMetValLeuAspSerGlyArg 1251

Db       4456 GCTCATCGGCTGAATACCATAATGGACTATACAAGGGTGATTGTCCTGGACAAAGGAGAA 4515

Qy       1252 LeuLysGluTyrAspGluProTyrValLeuLeuGlnAsnLysGluSerLeuPheTyrLys 1271

Db       4516 ATTCGGGAGTGTGGTGCACCCTCTGAGCTCCTGCAGCAAAGA---GGCGTCTTCTATAGC 4572

Qy       1272 MetValGlnGlnLeuGly 1277

Db       4573 ATGGCCAAGGATGCTGGC 4590
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RESULT 12
US-10-932-182A-484
; Sequence 484, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 484
; LENGTH: 4551
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-484

Alignment Scores:

Pred. No.:	1.09e-203	Length:	4551
Score:	2227.00	Matches:	499
Percent Similarity:	56.6%	Conservative:	256
Best Local Similarity:	37.4%	Mismatches:	497
Query Match:	32.8%	Indels:	82
DB:	7	Gaps:	23

US-09-976-858-42 (1-1325) x US-10-932-182A-484 (1-4551)

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Qy          4 ValTyrGlnGluVal---------LysProAsnProLeuGlnAspAlaAsnLeuCysSer 20

Db        598 ATACATCAGAAGTTGATGAGAAGGAAACCGAACCCGTACGATAGTGCTAATATATTCTCC 657

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40

Db        658 AGAATTACATTTTCTTGGATGTCAGGTTTAATGAAAACTGGATATGAAAAATACCTAGTA 717

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60

Db        718 GAAGCTGATTTGTATAAATTACCAAAAAACTTTAGTAGCACAGAACTCTCTCAGAAATTA 777

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80

Db        778 GAGAAAAATTGGCAAAATGAACTT------------AAGCATAAATCAAAGCCTTCGTTA 825

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100

Db        826 TCTTGGGCTATATGCAAAACTTTTGGATATAAAATGGTTTTAGCCGCGTTCTTCAAAGCC 885

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120

Db        886 ATTCATGATATTCTGGCATTCGTGCAACCACAATTACTAAGAATTTTAATCAAGTTTGTT 945

Qy        121 GluAsnTyr------------------------AspProMet---------------Asp 127

Db        946 ACCGACTACAATAAAGAAAGACAAGATGATGACGATCCTTTAACTCTCGGATATGGTGAT 1005

Qy        128 SerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThrLeuIle 147

Db       1006 AAGCCTGATCAAAAATTGCCCATTATAAGAGGTTTTATGATTGCGTTTTCCATGTTCTTG 1065

Qy        148 LeuAlaIleLeuHis------------HisLeuTyrPheTyrHisValGlnCysAlaGly 163

Db       1066 GTTGGGTTTACTCAAACATCTGTGCTGCATCAATATTTTTGAATGTCTTTAACACTGGT 1125

Qy        164 MetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsn 183

Db       1126 ATGTATGTCAAAAGTGCCTTGACTGCCTTGATATACCAAAAGGCTTTAGTTTTATCTAAT 1185

Qy        184 MetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsn 203

Db       1186 GAAGCATCTGGACTTTCATCTACTGGTGACATCGTTAATTTAATGAGCGTGGATGTCCAA 1245

Qy        204 LysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIle 223

Db       1246 AAATTACAAGATCTGACTCAATGGTTAAATTTGATTTGGTCAGGGCCCTTTCAGATTATT 1305

Qy        224 AlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaVal 243

Db       1306 ATCTGTCTCTACTCTTTGTATAAGCTATTGGGTAATTCGATGTGGGTTGGTGTAATCATA 1365

Qy        244 LeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSer 263

Db       1366 CTAGTTGTTATGATGCCATTAAATTCATTTTTAATGAGAATACAAAAGAAATTACAAAAA 1425

Qy        264 LysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIle 283

Db       1426 TCTCAAATGAAATACAAAGACGAAAGAACTCGTGTTATTAGTGAAATTCTAAACAACATC 1485
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Qy        284 ArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArg 303
              :::   :::|||:::|||||||||||||     :::          :::   ::::::|||
Db       1486 AAATCTCTGAAATTATATGCGTGGGAAAAGCCTTACAGGGAGAAGTTGGAAGACGTTAGA 1545

Qy        304 ---LysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAla 322
                 ||||||::::::   :::    :::      |||          :::
Db       1546 AATAACAAAGAACTAAATAATTTAACTAAATTGGGTTGCTATATGGCTGTAACAAGTTTC 1605

Qy        323 SerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeu 342
                 |||             ::::::         ||||||         :::|||
Db       1606 CAATTTAACATAGTTCCTTTCCTAGTTTCATGCTGTACGTTTGCTGTCTTTGTGTACACC 1665

Qy        343 ---GlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaVal 361
                       :::|||          ||||||   |||:::||||||:::       :::
Db       1666 GAAGATAGGGCCTTGACTACCGATCTAGTTTTCCCTGCTTTAACTCTTTTCAATCTACTT 1725

Qy        362 ArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleVal 381
                       :::   :::      |||      :::         ||||||   |||
Db       1726 TCATTTCCATTG---ATGATTATTCCCATGGTTTTGAATTCATTATCGAAGCTTCTGTT 1782

Qy        382 SerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSer-----------Gln 397
              ||||||   |||:::   :::|||         :::|||:::                |||
Db       1783 TCTATTGGTAGGCTATTTTCCTTTTTTACCAATGAGGAGCTACAGCCAGATTCTGTTCAG 1842

Qy        398 ArgAsnArgGlnLeuProSerAspGlyLysLysMetValHisVal---GlnAspPheThr 416
              |||      ::::::   :::   |||      :::::::::      |||   |||
Db       1843 CGCTTACCAAAAGTAGAAAATGTTGGTGATATAGCCATCAATATTGGCGACGACGCTACC 1902

Qy        417 AlaPheTrpAspLysAlaSerGlu---ThrProThrLeuGlnGlyLeuSerPheThrVal 435
                    |||   :::      |||            |||:::   ::::::|||
Db       1903 TTTTTATGGCAACGTAAACCAGAATATAAAGTAGCGTTGAAAAATATCAATTTCCAAGCT 1962

Qy        436 ArgProGlyGluLeuLeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeu 455
              :::   |||||||||      :::||||||   ||||||:::||||||::::::||||||
Db       1963 AAGAAAGGAGAATTAACCTGTATTGTTGGTAAGGTTGGTAGTGGGAAGACCGCTCTATTA 2022

Qy        456 SerAlaValLeuGlyGluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIle 475
              |||:::   ||||||:::|||            |||      ||||||||||||   :::
Db       2023 TCAAGCACATTGGGTGACTTATTTAGAGTCAAAGGGTTTGCCTCAGTGCACGGTAGTGTT 2082

Qy        476 AlaTyrValSerGlnGlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPhe 495
              ||||||||||||||   ||||||:::   ||||||||||::::::   ||||||||||||
Db       2083 GCATACGTCTCACAAGTTCCATGGATTATGAATGGGACGGTCAAGGAAAACATTTTGTTT 2142

Qy        496 GlyLysLysTyrGluLysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLys 515
              |||   ||||||:::   :::   |||||||||   ||||||||||||||||||
Db       2143 GGCATAAGTACGATGCTGACTTTTATGAAAAAACTATCAAGGCCTGTGCGTTAACCATT 2202

Qy        516 AspLeuGlnLeuLeuGluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeu 535
              ||||||   :::|||   |||||||||   |||::::::|||::::::|||   :::|||
Db       2203 GACTTGGCAATTTTGATGGATGGTGATAAGACGCTAGTTGGTGAAAAGGGTATTTCCTTG 2262

Qy        536 SerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIle 555
              |||||||||||||||||||||||::::::||||||||||||||||||      ||||||
Db       2263 TCGGGCGGCCAAAAGGCACGTCTATCCTTAGCAAGAGCAGTTTATTCAAGGGCAGATACT 2322

Qy        556 TyrLeuLeuAspAspProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGlu 575
              ||||||||||||||||||||||||:::||||||||| |||   :::||||||
Db       2323 TATCTACTGGACGATCCCTTGGCGGCTGTTGACGAACACGTGGCTAGGCATTTGGTCAAA 2382

Qy        576 LeuCysIleCysGln------IleLeuHisGluLysIleThrIleLeuValThrHisGln 593
                 :::                :::||||||   |||      :::|||   |||::::::
Db       2383 CATGTATTGGGTTCAAATGGTTTACTACATTCCAAAACCAAGTTATTGGCAACGAACAAA 2442

Qy        594 LeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIleLeuLysAspGlyLysMetValGln 613
              :::      |||      |||      |||   :::|||   :::|||:::::::::|||
Db       2443 GTAAGCGCCTTATCTGTTGCAGATTCAATTGCATTATTAGATAATGGTGAAATTATTCAA 2502

Qy        614 LysGlyThrTyrThrGluPheLeuLysSerGly-----------------------Ile 625
              :::||||||||||   :::      |||
Db       2503 CAAGGGACATATGATGATATTACCAAGGACGCGGACTCTCCCTTGTGGAAATTAATCAAC 2562

Qy        626 AspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProProValProGly 645
              |||:::|||        ||||||   |||:            :::
Db       2563 GATTATGGT---------AAAAAACACAATAATACACACAGCGAAACCAGTGAATCTTCA 2613

Qy        646 ThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGlnGlnSerSer 665
              |||   :::::::|||      :::                     |||
Db       2614 ACTAACTCAATTCGCGAAAACAGTATACCGATTGAAGGCGAGCTGGAACAATTACAAAAA 2673

Qy        666 ArgProSerLeuLysAspGlyAlaLeuGluSerGln----------------------- 677
                    |||      |||   ::::::|||
Db       2674 CTAAATGATCTGGATTTCGGCAACGCTGACACTCAAAGCTTAAGAAGAGCTAGTGATGCA 2733

Qy        678 -----------------------AspThrGluAsnValProValThrLeuSerGluGlu 689
                                     |||   |||||||||                  |||
Db       2734 ACTTTACGCAGTATTGATTTTGGCGATGATGAAAACGTT---------GCTAAAAGAGAA 2784

Qy        690 AsnArgSerGluGlyLysValGlyPheGlnAlaTyrLysAsnTyrPheArgAlaGlyAla 709
              :::|||   :::|||||||||   :::         |||      |||   :::|||
Db       2785 CATCGTGAACAGGGGAAGGTGAAGTGGAACATTTACCTAGAGTACGCTAAAGCTTGTAAC 2844

Qy        710 HisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAlaAlaGlnValAlaTyrVal 729
                    |||   :::|||::::::   :::         :::               |||
Db       2845 CCAAAAAGTGTTTGTGTGTTCATATTGTTTATC---GTTATATCAATGTTCCTATCCGTC 2901

Qy        730 LeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMetLeuAsnValThrVal 749
              :::   :::   ||||||   :::|||:::            |||
Db       2902 ATGGGTAACGTTTGGTTGAAACACTGGTCCGAAGTTAATAGCCGCTATGGGGCTAATCCG 2961

Qy        750 AsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsnTrpTyrLeuGlyIleTyrSer 769
              |||                                       ||||||||||||||||||
Db       2962 AATGCTGCTCGT------------------------------TACTTGGGTATCTATTTC 2991

Qy        770 GlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeuValPhe---Tyr 788
                 |||   :::   :::   |||      :::   :::::::::::::::::::   |||
Db       2992 GCCCTTGGTATTGGTTCAGCGTTGGCAACTTTAATTCAGACTATTGTTCTTTGGGTCTAC 3051

Qy        789 ValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIleLeuLysAla 808
                    :::::::::|||:::      |||||||||   |||      |||:::|||:::|||
Db       3052 TGCACTATTCATGCCTCCAAATATTTGCACAACTTGATGACAAACTCTGTGCTAAGAGCT 3111

Qy        809 ProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArgPheSerLysAsp 828
              |||:::   ||||||:::         ||||||||||||||||||||||||   |||
Db       3112 CCAATGACCTTTTTCGAAACCACACCGATTGGTAGAATTTTAAACCGTTTTTCGAATGAT 3171

Qy        829 IleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGlnThrLeuLeu 848
              |||      :::|||   ||||||      |||      |||            :::
Db       3172 ATATATAAAGTTGATGCTTTGTTGGGAAGAACCTTTTCTCAGTTTTTGTGAATGCGGTA 3231

Qy        849 GlnValValGlyValValSerValAlaValAlaValIleProTrpIleAlaIleProLeu 868
              :::|||         ::::::|||      |||                        :::
Db       3232 AAAGTTACGTTTACTATTACTGTTATTTGTGCGACAACGTGGCAATTCATTTTTATAATC 3291

Qy        869 ValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGluThrSerArgAsp 888
              ||||||||||||:::   :::|||:::   ::::::|||:::|||   |||||||||:::
Db       3292 GTTCCATTGGGTGTGTTTTACATTTACTATCAACAGTACTATTTAAGGACATCAAGGGAG 3351

Qy        889 ValLysArgLeuGluSerThrThrArgSerProValPheSerHisLeuSerSerSerLeu 908
              ::::::||||||:::|||   ||||||||||||::::::||||||            :::|||
Db       3352 TTGCGTCGTTTAGATTCTATCACAAGGTCTCCAATTTATTCTCATTTTCAAGAAACTTTG 3411

Qy        909 GlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArgCysGlnGluLeuPheAsp 928
                 ||||||   |||:::|||   |||      ::::::|||         :::
Db       3412 GGCGGTCTTGCTACAGTTAGAGGTTATTCACAGCAAAAGAGATTTCACACATTAATCAA 3471

Qy        929 AlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSerArgTrpPhe 948
                    |||   :::      |||:::::::         :::         :::||||||
Db       3472 TGTCGTATTGATAATAACATGAGTGCGTTTTATCCTTCTGTCAATGCTAATCGTTGGTTG 3531

Qy        949 AlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPheGlySerLeu 968
              |||   ||||||:::   |||   ::::::   ::::::         |||      |||:::
Db       3532 GCATACAGATTGGAACTTATTGGTTCTGTTATTATTTGGGCGCTGCTACTTTATCGGTT 3591

Qy        969 IleLeuAlaLys------ThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyrAla 986
                    |||            ||||||   ||||||   |||||||||:::||||||||||||
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Db       3592 TTCAGGCTAAAGCAAGGTACCTTGACTGCGGGTATGGTTGGTTTGTCGCTAAGTTATGCA 3651

Qy        987 LeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGluValGluAsnMet 1006
              |||   :::                |||    ||||||    :::   |||||||||
Db       3652 TTACAAATCACCCAAACATTGAATTGGATTGTTAGAATGACCGTTGAAGTGGAAACCAAT 3711

Qy       1007 MetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGluAlaProTrpGlu 1026
              :::::|||||||||||||:::    ||||||  ||||||:::   |||||||||
Db       3712 ATTGTTTCGGTGGAGAGAATTAAAGAATACGCTGACTTAAAGAGTGAGGCGCCCTTAGTT 3771

Qy       1027 TyrGln---LysArgProProProAlaTrpProHisGluGlyValIleIlePheAspAsn 1045
               :::     |||||||||      ||||||    :::|||   |||   |||:::
Db       3772 ATCGAAGGTCACAGGCCACCCAAGGAATGGCCAGGCCAAGGTGACATCAAGTTCAATCAA 3831

Qy       1046 ValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIle 1065
               :::     |||   |||       |||||||||||     :::           |||
Db       3832 TATTCCACTCGTTATAGACCAGAGCTTGATCTTGTTCTGAAACAGATTGATATTCACATC 3891

Qy       1066 LysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeuIle 1085
              |||   :::||||||:::||||||||||||||||||||||||||||||||||||||||
Db       3892 AAACCGAAGGAAAAAATTGGTATTGTTGGTAGAACAGGTGCAGGTAAATCGTCGTTAACA 3951

Qy       1086 SerAlaLeuPheArgLeuSerGluProGlu---GlyLysIleTrpIleAspLysIleLeu 1104
              ||||||||||||:::   |||              |||   |||   ||||||   |||
Db       3952 TTAGCGCTATTCAGAATCATTGAAGCTAGTGCGGGAAATATTGTTATTGATGACATTCCC 4011

Qy       1105 ThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGluPro 1124
                 |||||||||||||:::|||||||||     |||:::||||||||||||||||:::
Db       4012 ATTAATGAAATTGGGTTATATGACTTAAGACATAAACTGTCCATTATACCTCAAGATTCC 4071

Qy       1125 ValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThrAspGlu 1144
                 :::|||     ||||||:::|||:::|||:::||||||   |||::::::||||||||
Db       4072 CAAGTGTTTGAAGGTACTGTTCGTGAGAATATCGATCCAATCAACCAATACACCGATGAG 4131

Qy       1145 GluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGly 1164
                 :::|||   ||||||:::         |||||||||    :::      :::
Db       4132 GCTATGTGGAGAGCATTGGAACTTTCTCATTTGAAAGAACATGTGTTATCAATGAGTAAC 4191

Qy       1165 Lys---MetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGlnArgGln 1183
                 :::|||::::::|||   |||   |||||||||    ||||||||||||||||||
Db       4192 GATGGGTTAGACTCTCAATTAACAGAAGGTGGTAGTAACCTAAGTGTGGGACAAAGACAA 4251

Qy       1184 LeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAla 1203
              |||:::||||||||||||||||:::|||          ::::::||||||::::::|||||||||
Db       4252 TTACTGTGTCTTGCGAGAGCAATGCTGGTTCCATCCAAAATTTTGGTGCTAGATGAAGCC 4311

Qy       1204 ThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPhe 1223
              ||||||   ||||||         ||||||   :::||||||:::   ||||||      |||
Db       4312 ACCGCTGCAGTGGATGTCGAAACAGATAGAGTCATTCAAGAGACAATTCGCACGGCCTTT 4371

Qy       1224 AlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLys 1243
                       |||:::||||||||||||||||||||||||||||||:::||||||||:::
Db       4372 AGAGATAGAACTATATTGACTATCGCACACAGGTTGAACACCATCATGGATAGCGATAGA 4431

Qy       1244 IleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGln 1263
              |||:::|||||||||:::|||::::::   |||:::|||   |||      ||||||
Db       4432 ATCATTGTGTTGGATAACGGTAAAGTGGCTGAGTTTGATTCCCCATCCCAGCTATTAACC 4491

Qy       1264 AsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGly 1277
              |||   :::|||||||||||||    :::        :::   |||
Db       4492 AATACCAAATCATTATTCTATTCGTTGTGCACGGAAGCCGGT 4533
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RESULT 13
US-10-932-182A-484
; Sequence 484, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 484
; LENGTH: 4551
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-484

Alignment Scores:

Pred. No.:	1.09e-203	Length:	4551
Score:	2227.00	Matches:	499
Percent Similarity:	56.6%	Conservative:	256
Best Local Similarity:	37.4%	Mismatches:	497
Query Match:	32.8%	Indels:	82
DB:	7	Gaps:	23

US-09-976-858-42 (1-1325) x US-10-932-182A-484 (1-4551)

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Qy          4 ValTyrGlnGluVal---------LysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
              ::::::|||::::::             |||||||||||          ||||||:::   |||
Db        598 ATACATCAGAAGTTGATGAGAAGGAAACCGAACCCGTACGATAGTGCTAATATATTCTCC 657

Qy         21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
              |||:::   |||   |||::::::   |||   |||   |||:::::::::   |||
Db        658 AGAATTACATTTTCTTGGATGTCAGGTTTAATGAAAACTGGATATGAAAAATACCTAGTA 717

Qy         41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
              |||   |||:::|||   :::                  |||   |||   ::::::|||
Db        718 GAAGCTGATTTGTATAAATTACCAAAAAACTTTAGTAGCACAGAACTCTCTCAGAAATTA 777

Qy         61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
              :::      |||      |||:::                      ||||||||||||
Db        778 GAGAAAAATTGGCAAAATGAACTT------------AAGCATAAATCAAAGCCTTCGTTA 825

Qy         81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
              :::   ||||||   |||   :::         ::::::          |||
Db        826 TCTTGGGCTATATGCAAAACTTTTGGATATAAAATGGTTTTAGCCGCGTTCTTCAAAGCC 885

Qy        101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
              |||   :::         :::||||||      |||      :::|||   :::
Db        886 ATTCATGATATTCTGGCATTCGTGCAACCACAATTACTAAGAATTTTAATCAAGTTTGTT 945

Qy        121 GluAsnTyr-----------------------AspProMet---------------Asp 127
                 :::|||                       ||||||:::                |||
Db        946 ACCGACTACAATAAAGAAAGACAAGATGATGACGATCCTTTAACTCTCGGATATGGTGAT 1005

Qy        128 SerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThrLeuIle 147
                                                   ::::::   |||         :::
Db       1006 AAGCCTGATCAAAAAATTGCCCATTATAAGAGGTTTTATGATTGCGTTTTCCATGTTCTTG 1065

Qy        148 LeuAlaIleLeuHis------------HisLeuTyrPheTyrHisValGlnCysAlaGly 163
              :::                        |||. ||||||   :::|||         |||
Db       1066 GTTGGGTTTACTCAAACATCTGTGCTGCATCAATATTTTTGAATGTCTTTAACACTGGT 1125

Qy        164 MetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsn 183
              |||   ::::::   |||:::         :::||||||:::|||||||||   |||||||||
Db       1126 ATGTATGTCAAAAGTGCCTTGACTGCCTTGATATACCAAAAGGCTTTAGTTTTATCTAAT 1185

Qy        184 MetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsn 203
                 |||   |||   ::::::||||||   ||||||||||||:::|||   ||||||
Db       1186 GAAGCATCTGGACTTTCATCTACTGGTGACATCGTTAATTTAATGAGCGTGGATGTCCAA 1245

Qy        204 LysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAlaIle 223
              |||         :::|||   :::|||:::   :::|||:::||||||   |||   |||
Db       1246 AAATTACAAGATCTGACTCAATGGTTAAATTTGATTTGGTCAGGGCCCTTTCAGATTATT 1305

Qy        224 AlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAlaVal 243
                          |||:::         :::|||   |||         |||:::   :::
Db       1306 ATCTGTCTCTACTCTTTGTATAAGCTATTGGGTAATTCGATGTGGGTTGGTGTAATCATA 1365
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Qy        244 LeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSer 263
Db       1366 CTAGTTGTTATGATGCCATTAAATTCATTTTTAATGAGAATACAAAAGAAATTACAAAAA 1425
Qy        264 LysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIle 283
Db       1426 TCTCAAATGAAATACAAAGACGAAAGAACTCGTGTTATTAGTGAAATTCTAAACAACATC 1485
Qy        284 ArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArg 303
Db       1486 AAATCTCTGAAATTATATGCGTGGGAAAAGCCTTACAGGGAGAAGTTGGAAGACGTTAGA 1545
Qy        304 ---LysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeuAla 322
Db       1546 AATAACAAAGAACTAAATAATTTAACTAAATTGGGTTGCTATATGGCTGTAACAAGTTTC 1605
Qy        323 SerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeuLeu 342
Db       1606 CAATTTAACATAGTTCCTTTCCTAGTTTCATGCTGTACGTTTGCTGTCTTTGTGTACACC 1665
Qy        343 ---GlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAlaVal 361
Db       1666 GAAGATAGGGCCTTGACTACCGATCTAGTTTTCCCTGCTTTAACTCTTTTCAATCTACTT 1725
Qy        362 ArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleVal 381
Db       1726 TCATTTCCATTG---ATGATTATTCCCATGGTTTTGAATTCATTTATCGAAGCTTCTGTT 1782
Qy        382 SerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSer------------Gln 397
Db       1783 TCTATTGGTAGGCTATTTTCCTTTTTTACCAATGAGGAGCTACAGCCAGATTCTGTTCAG 1842
Qy        398 ArgAsnArgGlnLeuProSerAspGlyLysLysMetValHisVal---GlnAspPheThr 416
Db       1843 CGCTTACCAAAAGTAGAAAATGTTGGTGATATAGCCATCAATATTGGCGACGACGCTACC 1902
Qy        417 AlaPheTrpAspLysAlaSerGlu---ThrProThrLeuGlnGlyLeuSerPheThrVal 435
Db       1903 TTTTTATGGCAACGTAAACCAGAATATAAAGTAGCGTTGAAAAATATCAATTTCCAAGCT 1962
Qy        436 ArgProGlyGluLeuLeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeu 455
Db       1963 AAGAAAGGAGAATTAACCTGTATTGTTGGTAAGGTTGGTAGTGGGAAGACCGCTCTATTA 2022
Qy        456 SerAlaValLeuGlyGluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIle 475
Db       2023 TCAAGCACATTGGGTGACTTATTTAGAGTCAAAGGGTTTGCCTCAGTGCACGGTAGTGTT 2082
Qy        476 AlaTyrValSerGlnGlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPhe 495
Db       2083 GCATACGTCTCACAAGTTCCATGGATTATGAATGGGACGGTCAAGGAAAACATTTTGTTT 2142
Qy        496 GlyLysLysTyrGluLysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLys 515
Db       2143 GGGCATAAGTACGATGCTGACTTTTATGAAAAAACTATCAAGGCCTGTGCGTTAACCATT 2202
Qy        516 AspLeuGlnLeuLeuGluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeu 535
Db       2203 GACTTGGCAATTTTGATGGATGGTGATAAGACGCTAGTTGGTGAAAAGGGTATTTCCTTG 2262
Qy        536 SerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIle 555
Db       2263 TCGGGCGGCCAAAAGGCACGTCTATCCTTAGCAAGAGCAGTTTATTCAAGGGCAGATACT 2322
Qy        556 TyrLeuLeuAspAspProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGlu 575
Db       2323 TATCTACTGGACGATCCCTTGGCGGCTGTTGACGAACACGTGGCTAGGCATTTGGTCAAA 2382
Qy        576 LeuCysIleCysGln------IleLeuHisGluLysIleThrIleLeuValThrHisGln 593
Db       2383 CATGTATTGGGTTCAAATGGTTTACTACATTCCAAAACCAAGTTATTGGCAACGAACAAA 2442
Qy        594 LeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIleLeuLysAspGlyLysMetValGln 613
Db       2443 GTAAGCGCCTTATCTGTTGCAGATTCAATTGCATTATTAGATAATGGTGAAATTATTCAA 2502
Qy        614 LysGlyThrTyrThrGluPheLeuLysSerGly-----------------------Ile 625
Db       2503 CAAGGGACATATGATGATATTACCAAGGACGCGGACTCTCCCTTGTGGAAATTAATCAAC 2562
Qy        626 AspPheGlySerLeuLeuLysLysAspAsnGluGluSerGluGlnProProValProGly 645
Db       2563 GATTATGGT---------AAAAAACACAATAATACACACAGCGAAACCAGTGAATCTTCA 2613
Qy        646 ThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGlnGlnSerSer 665
Db       2614 ACTAACTCAATTCGCGAAAACAGTATACCGATTGAAGGCGAGCTGGAACAATTACAAAAA 2673
Qy        666 ArgProSerLeuLysAspGlyAlaLeuGluSerGln----------------------- 677
Db       2674 CTAAATGATCTGGATTTCGGCAACGCTGACACTCAAAGCTTAAGAAGAGCTAGTGATGCA 2733
Qy        678 -----------------------AspThrGluAsnValProValThrLeuSerGluGlu 689
Db       2734 ACTTTACGCAGTATTGATTTTGGCGATGATGAAAACGTT---------GCTAAAAGAGAA 2784
Qy        690 AsnArgSerGluGlyLysValGlyPheGlnAlaTyrLysAsnTyrPheArgAlaGlyAla 709
Db       2785 CATCGTGAACAGGGGAAGGTGAAGTGGAACATTTACCTAGAGTACGCTAAAGCTTGTAAC 2844
Qy        710 HisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAlaAlaGlnValAlaTyrVal 729
Db       2845 CCAAAAAGTGTTTGTGTGTTCATATTGTTTATC---GTTATATCAATGTTCCTATCCGTC 2901
Qy        730 LeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMetLeuAsnValThrVal 749
Db       2902 ATGGGTAACGTTTGGTTGAAACACTGGTCCGAAGTTAATAGCCGCTATGGGGCTAATCCG 2961
Qy        750 AsnGlyGlyGlyAsnValThrGluLysLeuAspLeuAsnTrpTyrLeuGlyIleTyrSer 769
Db       2962 AATGCTGCTCGT-----------------------------TACTTGGGTATCTATTTC 2991
Qy        770 GlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeuValPhe---Tyr 788
Db       2992 GCCCTTGGTATTGGTTCAGCGTTGGCAACTTTAATTCAGACTATTGTTCTTTGGGTCTAC 3051
Qy        789 ValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIleLeuLysAla 808
Db       3052 TGCACTATTCATGCCTCCAAATATTTGCACAACTTGATGACAAACTCTGTGCTAAGAGCT 3111
Qy        809 ProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArgPheSerLysAsp 828
Db       3112 CCAATGACCTTTTTCGAAACCACACCGATTGGTAGAATTTTAAACCGTTTTTCGAATGAT 3171
Qy        829 IleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGlnThrLeuLeu 848
Db       3172 ATATATAAAGTTGATGCTTTGTTGGGAAGAACCTTTTCTCAGTTTTTTGTGAATGCGGTA 3231
Qy        849 GlnValValGlyValValSerValAlaValAlaValIleProTrpIleAlaIleProLeu 868
Db       3232 AAAGTTACGTTTACTATTACTGTTATTTGTGCGACAACGTGGCAATTCATTTTTATAATC 3291
Qy        869 ValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGluThrSerArgAsp 888
Db       3292 GTTCCATTGGGTGTGTTTTACATTTACTATCAACAGTACTATTTAAGGACATCAAGGGAG 3351
Qy        889 ValLysArgLeuGluSerThrThrArgSerProValPheSerHisLeuSerSerSerLeu 908
Db       3352 TTGCGTCGTTTAGATTCTATCACAAGGTCTCCAATTTATTCTCATTTTCAAGAAACTTTG 3411
Qy        909 GlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArgCysGlnGluLeuPheAsp 928
Db       3412 GGCGGTCTTGCTACAGTTAGAGGTTATTCACAGCAAAAGAGATTTTCACACATTAATCAA 3471
Qy        929 AlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSerArgTrpPhe 948
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Db       3472 TGTCGTATTGATAATAACATGAGTGCGTTTTATCCTTCTGTCAATGCTAATCGTTGGTTG 3531

Qy        949 AlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPheGlySerLeu 968
Db       3532 GCATACAGATTGGAACTTATTGGTTCTGTTATTATTTGGGCGCTGCTACTTTATCGGTT 3591

Qy        969 IleLeuAlaLys------ThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyrAla 986
Db       3592 TTCAGGCTAAAGCAAGGTACCTTGACTGCGGGTATGGTTGGTTTGTCGCTAAGTTATGCA 3651

Qy        987 LeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGluValGluAsnMet 1006
Db       3652 TTACAAATCACCCAAACATTGAATTGGATTGTTAGAATGACCGTTGAAGTGGAAACCAAT 3711

Qy       1007 MetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGluAlaProTrpGlu 1026
Db       3712 ATTGTTTCGGTGGAGAGAATTAAAGAATACGCTGACTTAAAGAGTGAGGCGCCCTTAGTT 3771

Qy       1027 TyrGln---LysArgProProProAlaTrpProHisGluGlyValIleIlePheAspAsn 1045
Db       3772 ATCGAAGGTCACAGGCCACCCAAGGAATGGCCAGGCCAAGGTGACATCAAGTTCAATCAA 3831

Qy       1046 ValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIle 1065
Db       3832 TATTCCACTCGTTATAGACCAGAGCTTGATCTTGTTCTGAAACAGATTGATATTCACATC 3891

Qy       1066 LysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeuIle 1085
Db       3892 AAACCGAAGGAAAAAATTGGTATTGTTGGTAGAACAGGTGCAGGTAAATCGTCGTTAACA 3951

Qy       1086 SerAlaLeuPheArgLeuSerGluProGlu---GlyLysIleTrpIleAspLysIleLeu 1104
Db       3952 TTAGCGCTATTCAGAATCATTGAAGCTAGTGCGGGAAATATTGTTATTGATGACATTCCC 4011

Qy       1105 ThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGluPro 1124
Db       4012 ATTAATGAAATTGGGTTATATGACTTAAGACATAAACTGTCCATTATACCTCAAGATTCC 4071

Qy       1125 ValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThrAspGlu 1144
Db       4072 CAAGTGTTTGAAGGTACTGTTCGTGAGAATATCGATCCAATCAACCAATACACCGATGAG 4131

Qy       1145 GluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGly 1164
Db       4132 GCTATGTGGAGAGCATTGGAACTTTCTCATTTGAAAGAACATGTGTTATCAATGAGTAAC 4191

Qy       1165 Lys---MetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGlyGlnArgGln 1183
Db       4192 GATGGGTTAGACTCTCAATTAACAGAAGGTGGTAGTAACCTAAGTGTGGGACAAAGACAA 4251

Qy       1184 LeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAla 1203
Db       4252 TTACTGTGTCTTGCGAGAGCAATGCTGGTTCCATCCAAAATTTTGGTGCTAGATGAAGCC 4311

Qy       1204 ThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPhe 1223
Db       4312 ACCGCTGCAGTGGATGTCGAAACAGATAGAGTCATTCAAGAGACAATTCGCACGGCCTTT 4371

Qy       1224 AlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLys 1243
Db       4372 AGAGATAGAACTATATTGACTATCGCACACAGGTTGAACACCATCATGGATAGCGATAGA 4431

Qy       1244 IleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGln 1263
Db       4432 ATCATTGTGTTGGATAACGGTAAAGTGGCTGAGTTTGATTCCCCATCCCAGCTATTAACC 4491

Qy       1264 AsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGly 1277
Db       4492 AATACCAAATCATTATTCTATTCGTTGTGCACGGAAGCCGGT 4533
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RESULT 14
US-11-136-527-2145
; Sequence 2145, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2145
; LENGTH: 4954
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2145

Alignment Scores:

Pred. No.:	3.95e-201	Length:	4954
Score:	2201.00	Matches:	495
Percent Similarity:	55.7%	Conservative:	266
Best Local Similarity:	36.2%	Mismatches:	478
Query Match:	32.4%	Indels:	128
DB:	12	Gaps:	24

US-09-976-858-42 (1-1325) x US-11-136-527-2145 (1-4954)

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Qy         12 ProLeuGlnAspAlaAsnLeuCysSerArgValPhePheTrpTrpLeuAsnProLeuPhe 31
Db        671 CCATCAGTCACGGCTTCCTTTCTGAGTAGCATTACATTTAGTTGGTATGACAGGACTGTT 730

Qy         32 LysIleGlyHisLysArgArgLeuGluGluAspAspMetTyrSerValLeuProGluAsp 51
Db        731 CTGAAAGGTTACAAGCATCCACTGACACTAGAAGATGTCTGGGATATCGATGAAGGGTTT 790

Qy         52 ArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheTrpAspLysGluValLeuArgAla 71
Db        791 AAAACAAGGTCAGTCACCAGCAAGTTTGAGGCGGCCATGACAAAGGACCTGCAGAAAGCC 850

Qy         72 ------------------------GluAsnAspAlaGlnLysProSerLeuThr------ 81
Db        851 AGGCAGGCTTTTCAGAGGCGGCTGCAGAAGTCCCAGCGGAAACCTGAGGCCACACTACAC 910

Qy         81 ------------------------------------------------------------ 81
Db        911 GGACTGAACAAGAAGCAGAGTCAGAGCCAAGACGTTCTCGTCCTGGAAGAAGCGAAAAAG 970

Qy         82 ------ArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePhe--- 98
Db        971 AAGTCTGAGAAGACCACCAAAGACTATCCCAAATCGTGGTTGATCAAGTCTCTCTTCAAA 1030

Qy         99 ------------------------------------ThrLeuIleGluGluSerAlaLys 106
Db       1031 ACCTTCCACGTAGTGATCCTGAAATCATTTATACTGAAATTAATACATGACCTTTTGGTG 1090

Qy        107 ValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspProMet 126
Db       1091 TTTCTGAATCCTCAGCTGCTGAAGTTGCTGATCGGTTTC--------------------- 1129

Qy        127 AspSerValAlaLeuAsnThrAlaTyrAlaTyr------------AlaThrValLeuThr 142
Db       1130 ------GTGAAGAGCTCTAACTCATACGTGTGGTTTGGCTATATCTGTGCAATCCTAATG 1183

Qy        143 PheCys---ThrLeuIleLeuAlaIleLeuHisHisLeuTyrPheTyrHisValGlnCys 161
Db       1184 TTTGCTGTGACTCTCATCCAATCTTTCTGCCTTCAGTCTTACTTTCAACATTGTTTTGTG 1243

Qy        162 AlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeu 181
Db       1244 TTGGGAATGTGCGTACGGACAACCGTCATGTCTTCGATATATAAGAAGGCATTGACCCTA 1303

Qy        182 SerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAsp 201
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Db   1304 TCTAACTTGGCTAGGAAGCAGTACACCATTGGAGAGACGGTGAACTTGRTGTCTGTAGAT 1363

Qy    202 ValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGln 221
Db   1364 TCCCAGAAGCTAATGGATGCGACCAACTACATGCAGTTGGTGTGGTCAAGTGTTATACAG 1423

Qy    222 AlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMet 241
Db   1424 ATTACTTTGTCCATCTTCTTCCTGTGGAGAGAGTTGGGACCGTCCATCTTAGCAGGTGTT 1483

Qy    242 AlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeu 261
Db   1484 GGGGTTATGGTTCTCCTAATCCCAGTTAATGGAGTTCTGGCTACCAAGATCAGAAATATT 1543

Qy    262 ArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThr 281
Db   1544 CAGGTCCAAAATATGAAGAATAAAGACAAACGTTTAAAAATCATGAATGAGATTCTCAGT 1603

Qy    282 GlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThrAsn 301
Db   1604 GGAATCAAGATCCTGAAATACTTTGCCTGGGAACCTTCATTTCAAGAGCAAGTCCAGGGC 1663

Qy    302 LeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeu 321
Db   1664 ATTCGGAAGAAAGAACTCAAGAACTTGCTGCGGTTCGGCCAGCTGCAGAGTCTGCTGATC 1723

Qy    322 AlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrValLeu 341
Db   1724 TTCATTTTACAGATAACTCCAATCCTGGTGTCTGTGGTCACATTTTCTGTCTATGTCCTG 1783

Qy    342 LeuGlySer------ValIleThrAlaSerArgValPheValAlaValThrLeuTyrGly 359
Db   1784 GTGGATAGCGCCAATGTTTTGAATGCGGAGAAGGCATTTACCTCCATCACCCTCTTCAAT 1843

Qy    360 AlaValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAla 379
Db   1844 ATCCTACGCTTCCCTCTGTCCATG---CTTCCCATGGTGACCTCATCGATCCTCCAGGCC 1900

Qy    380 IleValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsn 399
Db   1901 AGTGTTTCTGTGGACCGGCTGGAGAGGTATTTGGGAGGAGACGATTTAGACACATCTGCC 1960

Qy    400 ArgGlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrp 419
Db   1961 ATTCGCCGCGTCAGCAATTTTGATAAAGCTGTGAAGTTTTCAGAGGCCTCTTTTACTTGG 2020

Qy    420 AspLysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGlu 439
Db   2021 GACCCGGACTTGGAAGCC---ACAATCCAAGATGTGAACCTGGACATAAAGCCAGGCCAA 2077

Qy    440 LeuLeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeu 459
Db   2078 CTGGTGGCTGTGGTGGGCACTGTAGGCTCTGGGAAATCCTCTTTGGTATCAGCCATGCTG 2137

Qy    460 GlyGluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSer 479
Db   2138 GGAGAAATGGAAAACGTTCACGGGCACATCACCATCCAGGGATCCACAGCCTATGTCCCT 2197

Qy    480 GlnGlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyr 499
Db   2198 CAGCAGTCCTGGATTCAGAATGGAACCATCAAAGACAACATCCTGTTTGGGTCCGAATAC 2257

Qy    500 GluLysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeu 519
Db   2258 AATGAAAAGAAGTACCAGCAAGTTCTCAAAGCATGCGCTCTCCTCCCAGACTTGGAAATA 2317

Qy    520 LeuGluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGln 539
Db   2318 TTGCCTGGAGGAGACATGGCTGAGATCGGAGAGAAGGGGATAAATCTCAGTGGTGGTCAG 2377

Qy    540 LysAlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAsp 559
Db   2378 AAGCAGCGAGTCAGCCTGGCCAGAGCTGCCTATCAAGATGCTGACATCTATATTCTGGAC 2437

Qy    560 AspProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCys 579
Db   2438 GATCCCCTGTCGGCTGTGGATGCTCATGTGGGAAAACACATTTTCAACAAGGTTGTGGGC 2497

Qy    580 Gln------IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeu 597
Db   2498 CCCAACGGCCTGTTGGCTGGCAAGACGAGAATCTTTGTTACTCATGGTATTCACTTCCTT 2557

Qy    598 LysAlaAlaSerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyr 617
Db   2558 CCCCAAGTGGATGAGATTGTAGTTCTGGGGAAAGGCACCATCTTAGAGAAAGGATCCTAT 2617

Qy    618 ThrGluPheLeu---LysSerGlyIle---------AspPheGlySerLeuLeuLysLys 633
Db   2618 CGTGACCTGTTGGACAAGAAGGGAGTGTTTGCTAGGAACTGGAAGACCTTCATGAAGCAT 2677

Qy    634 AspAsnGluGluSerGluGln----------------------------------------- 640
Db   2678 TCAGGGCCTGAAGGAGAGGCCACAGTCAATAATGACAGTGAGGCGGAAGACGACGATGAT 2737

Qy    641 ---------ProProValProGlyThrPro------------------------------ 647
Db   2738 GGGCTGATTCCCACCATGGAGGAAATCCCTGAGGATGCAGCTTCCTTGGCCATGAGAAGA 2797

Qy    648 ------ThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGlnGlnSerSer 665
Db   2798 GAAAATAGTCTTCGC---CGTACACTGAGCCGCAGC---------TCTAGGTCCAGCAGC 2845

Qy    666 Arg------ProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnValPro 683
Db   2846 CGACGTGGGAAGTCCCTCAAAAAC------------TCCTTGAAGATTAAAAATGTGAAT 2893

Qy    684 ValThrLeuSerGluGluAsnArgSerGlu----------------------------- 693
Db   2894 GTCTTGAAGGAGAAGGAAAAAGAAGTGGAAGGACAAAAACTAATTAAGAAAGAATTTGTG 2953

Qy    694 ------GlyLysValGlyPheGlnAlaTyrLysAsnTyrPheArgAlaGlyAlaHisTrp 711
Db   2954 GAAACCGGGAAGGTCAAGTTCTCCATCTACCTGAAGTATCTACAGGCAGTAGGGTGGTGG 3013

Qy    712 IleValPheIlePheLeuIleLeuLeuAsnThrAlaAlaGlnValAlaTyrValLeuGln 731
Db   3014 TCCATA---CTTTTCATCATCCTTTTCTACGGATTGAATAATGTTGCTTTTATCGGCTCT 3070

Qy    732 AspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMetLeuAsnValThrValAsnGly 751
Db   3071 AACCTCTGGCTGAGTGCTTGGACCAGTGACTCTGACAACTTG------------AATGGG 3118

Qy    752 GlyGlyAsnValThrGluLysLeuAspLeuAsnTrpTyrLeuGlyIleTyrSerGlyLeu 771
Db   3119 ACCAACAATTCGTCTTCTCATAGGGACATGAGA------ATTGGGGTCTTTGGAGCTCTG 3172

Qy    772 ThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeuValPheTyrValLeuVal 791
Db   3173 GGATTAGCACAAGGTATATGTTTGCTTATTTCAACTCTGTGGAGCATATATGCTTGCAGA 3232

Qy    792 AsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIleLeuLysAlaProValLeu 811
Db   3233 AATGCATCAAAAGCTTTGCACGGGCAGCTGTTAACCAACATCCTCCGGGCACCCATGAGG 3292

Qy    812 PhePheAspArgAsnProIleGlyArgIleLeuAsnArgPheSerLysAspIleGlyHis 831
Db   3293 TTTTTTGACACAACTCCCACAGGCCGGATTGTGAACAGATTTTCTGGTGATATTTCTACT 3352

Qy    832 LeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGlnThrLeuLeuGlnValVal 851
Db   3353 GTGGACGACTTGCTCCCCCAGACACTTCGAAGCTGGATGATGTGTTTCTTTGGCATCGCT 3412

Qy    852 GlyValValSerValAlaValAlaValIleProTrpIleAlaIleProLeuValProLeu 871
Db   3413 GGCACTCTTGTCATGATCTGCATGGCCACCCCAGTCTTCGCTATCATCATCATTCCTCTC 3472
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Qy    872 GlyIleIlePheIlePheLeuArgArgTyrPheLeuGluThrSerArgAspValLysArg 891
Db   3473 AGCATTCTTTATATTTCGGTGCAGGTTTTTATGTGGCTACTTCCCGCCAGCTGAGACGG 3532

Qy    892 LeuGluSerThrThrArgSerProValPheSerHisLeuSerSerSerLeuGlnGlyLeu 911
Db   3533 TTGGATTCTGTCACCAAATCTCCGATCTATTCTCACTTCAGTGAGACTGTCACAGGTTTG 3592

Qy    912 TrpThrIleArgAlaTyrLysAlaGluGluArgCysGlnGluLeuPheAspAlaHisGln 931
Db   3593 CCCATTATCCGTGCCTTTGAGCACCAGCAGCGATTTCTAGCTTGGAATGAGAAGCAGATT 3652

Qy    932 AspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSerArgTrpPheAlaValArg 951
Db   3653 GACATCAACCAGAAATGTGTCTTTTCCTGGATTACCTCCAACAGGTGGCTTGCAATTCGG 3712

Qy    952 LeuAspAlaIleCysAlaMetPheValIleIleValAlaPheGlySerLeuIleLeuAla 971
Db   3713 CTGGAGCTGGTTGGAAACTTGGTCGTCTTCTGTTCCGCCTTGCTGCTGGTTATTTATAGA 3772

Qy    972 LysThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyrAlaLeuThrLeuMetGly 991
Db   3773 AAAACCTTAACCGGGGACGTTGTGGGCTTTGTTCTGTCCAACGCCCTCAATATCACACAA 3832

Qy    992 MetPheGlnTrpCysValArgGlnSerAlaGluValGluAsnMetMetIleSerValGlu 1011
Db   3833 ACCTTGAACTGGCTAGTGAGGATGACGTCAGAAGCAGAGACCAACATTGTGGCAGTTGAG 3892

Qy   1012 ArgValIleGluTyrThrAspLeuGluLysGluAlaProTrpGluTyrGlnLysArgPro 1031
Db   3893 CGAATAAGTGAATACATAAATGTAGAGAATGAGGCGCCCTGGGTGACTGACAAGAGGCCT 3952

Qy   1032 ProProAlaTrpProHisGluGlyValIleIlePheAspAsnValAsnPheMetTyrSer 1051
Db   3953 CCGGCAGACTGGCCCAGACATGGTGAGATCCAGTTTAACAACTATCAAGTGCGGTATCGG 4012

Qy   1052 ProGlyGlyProLeuValLeuLysHisLeuThrAlaLeuIleLysSerGlnGluLysVal 1071
Db   4013 CCGGAGCTGGATCTGGTACTGAAAGGGATCACTTGTAACATCAAGAGCGGAGAGAAGGTC 4072

Qy   1072 GlyIleValGlyArgThrGlyAlaGlyLysSerSerLeuIleSerAlaLeuPheArgLeu 1091
Db   4073 GGCRTRGTGGGSMGGACTGGGGCTGGGAAATCATCCCTCACRARSTGCCTCTTCAGAATC 4132

Qy   1092 SerGluProGlu---GlyLysIleTrpIleAspLysIleLeuThrThrGluIleGlyLeu 1110
Db   4133 TTAGAGTCTGCGGGGGGCCAGATCATCATTGATGGGATAGATGTTGCCTCCATTGGACTG 4192

Qy   1111 HisAspLeuArgLysLysMetSerIleIleProGlnGluProValLeuPheThrGlyThr 1130
Db   4193 CACGACCTTCGAGAGAGGCTGACCATCATTCCCCAGGACCCCATTTTGTTCTCGGGGAGT 4252

Qy   1131 MetArgLysAsnLeuAspProPheAsnGluHisThrAspGluGluLeuTrpAsnAlaLeu 1150
Db   4253 CTGAGGATGAAYCTCGACCCTTTCAACAAATATTCAGATGAGGAGGTTTGGAGGGCCCTG 4312

Qy   1151 GlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLysMetAspThrGluLeu 1170
Db   4313 GAGTTGGCTCACCTCAGATCCTTTGTGTCTGGCCTACAGCTTGGGTTGTTATCCGAAGTG 4372

Qy   1171 AlaGluSerGlySerAsnPheSerValGlyGlnArgGlnLeuValCysLeuAlaArgAla 1190
Db   4373 ACAGAGGGTGGTGACAACCTGAGCATAGGGCAGAGGCAGCTCCTATGCCTGGGCAGGGCT 4432

Qy   1191 IleLeuArgLysAsnGlnIleLeuIleIleAspGluAlaThrAlaAsnValAspProArg 1210
Db   4433 GTGCTTCGAAAATCCAAAATCCTGGTCCTGGATGAAGCCACGGCTGCAGTGGATCTCGAG 4492

Qy   1211 ThrAspGluLeuIleGlnLysLysIleArgGluLysPheAlaHisCysThrValLeuThr 1230
Db   4493 ACGGATAGCCTCATTCAGACGACCATCCGAAAGGAGTTCTCCCAGTGCACGGKCATCACC 4552

Qy   1231 IleAlaHisArgLeuAsnThrIleIleAspSerAspLysIleMetValLeuAspSerGly 1250
Db   4553 ATCGCTCACAGGCTGCACACCATCATGGACAGTGACAAGATAATGGTCCTAGACAACGGG 4612

Qy   1251 ArgLeuLysGluTyrAspGluProTyrValLeuLeuGlnAsnLysGluSerLeuPheTyr 1270
Db   4613 AAGATTGTCGAGTATGGCAGTCCTGAAGAACTGCTGTCCAACAGAGGTTCC---TTCTAT 4669

Qy   1271 LysMetValGlnGlnLeuGly 1277
Db   4670 CTGATGGCCAAGGAAGCCGGC 4690
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RESULT 15
US-11-136-527-475
; Sequence 475, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 475
; LENGTH: 5189
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-475

Alignment Scores:

Pred. No.:	1.7e-198	Length:	5189
Score:	2174.00	Matches:	484
Percent Similarity:	56.1%	Conservative:	277
Best Local Similarity:	35.7%	Mismatches:	485
Query Match:	32.0%	Indels:	110
DB:	12	Gaps:	24

US-09-976-858-42 (1-1325) x US-11-136-527-475 (1-5189)

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Qy      3 ProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSerArgVal 22
Db    658 CCAGAGAATCTTGACACAAATCCTTGCCCAGAGGCCAGCGCTGGCTTCTTCTCCCGTCTG 717

Qy     23 PhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGluGluAsp 42
Db    718 TCTTTCTGGTGGTTCACAAAGCTTGCCATCCTTGGCTACCGACGTCCCCTGGAGGACAGT 777

Qy     43 AspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeuGlnGly 62
Db    778 GACCTCTGGTCTCTGTCTGAGGAGGACTGCTCTCACAAGGTGGTACAACGGCTACTGGAA 837

Qy     63 PheTrpAspLysGlu------------------------------------------- 67
Db    838 GCATGGCAAAAGCAGCAGACCCAAGCATCAGGGCCCCAGACTGCAGCCCTTGAGCCAAAG 897

Qy     68 ---------------------ValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
Db    898 ATCGCAGGTGAGGATGAGGTCCTGCTGAAGGCCCGCCCCAAGACCAAGAAGCCTTCCTTT 957

Qy     81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
Db    958 CTGAGGGCTTTGGTGAGAACCTTCACCTCCAGCTTGCTCATGGGTGCCTGCTTCAAGCTG 1017

Qy    101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120
Db   1018 ATCCAGGACCTGCTCTCCTTCATCAACCCACAGCTGCTCAGCATCCTCATCAGGTTTATT 1077

Qy    121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAla---------------Tyr 135
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Db  1078 TCT------GACCCC---------------------ACGGCCCCTACCTGGTGGGGCTTC 1110
Qy   136 AlaTyrAlaThrValLeuThrPheCysThrLeuIleLeuAlaIleLeuHisHisLeuTyr 155
Db  1111 TTGCTGGCCGGACTGATGTTCGTGAGCTCCACCATGCAGACATTGATCTTACACCAACAT 1170
Qy   156 PheTyrHisValGlnCysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyr 175
Db  1171 TACCACTGCATCTTTGTGATGGCCTTGAGGATACGGACTGCTATCATAGGCGTCATCTAC 1230
Qy   176 ArgLysAlaLeuArgLeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleVal 195
Db  1231 AGGAAGGCTCTGACCATCACCAACTCAGTCAAACGTGAGTACACTGTGGGAGAAATGGTC 1290
Qy   196 AsnLeuLeuSerAsnAspValAsnLysPheAspGlnValThrValPheLeuHisPheLeu 215
Db  1291 AACCTCATGTCGGTGGACGCCCAGCGCTTCATGGATGTCTCCCCATTCATCAACCTGCTG 1350
Qy   216 TrpAlaGlyProLeuGlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIle 235
Db  1351 TGGTCTGCACCTTTGCAGGTCATCCTGGCGATATACTTCCTCTGGCAGATCTTAGGCCCA 1410
Qy   236 SerCysLeuAlaGlyMetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGly 255
Db  1411 TCAGCCCTGGCTGGGGTGGCTGTGATAGTCTTGCTGATACCACTCAATGGAGCTGTGTCC 1470
Qy   256 LysLeuPheSerSerLeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThr 275
Db  1471 ATGAAAATGAAGACCTACCAGGTACAGCAAATGAAGTTCAAAGACTCCCGCATCAAACTG 1530
Qy   276 MetAsnGluValIleThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPhe 295
Db  1531 ATGAGTGAGATCCTGAATGGCATCAAAGTTCTGAAGCTGTACGCTTGGGAGCCCACCTTC 1590
Qy   296 SerAsnLeuIleThrAsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCys 315
Db  1591 TTGGAGCAGGTAGAAGGAATCAGGCAGGGTGAGCTCCAGCTACTGCGGAAGGGCGCCTAC 1650
Qy   316 LeuArgGlyMetAsnLeuAlaSerPhePheSerAlaSerLysIleIleValPheValThr 335
Db  1651 CTGCAGGCTATCTCTACCTTCATCTGGGTCTGCACCCCGTTTATGGTGACCCTGATCACC 1710
Qy   336 PheThrThrTyrValLeuLeu------GlySerValIleThrAlaSerArgValPheVal 353
Db  1711 CTCGGGGTGTACGTGTGTGTGGACAAGAACAATGTGCTGGATGCTGAGAAGGCCTTCGTG 1770
Qy   354 AlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePheProSerAlaIle 373
Db  1771 TCCCTGTCCTTGTTCAATATCTTAAAGATCCCCCTCAACCTG---CTGCCTCAGTTAATC 1827
Qy   374 GluArgValSerGluAlaIleValSerIleArgArgIleGlnThrPheLeuLeuLeuAsp 393
Db  1828 AGTGGCATGACCCAGACCAGCGTGTCTCTGAAACGGATCCAGGATTTCCTGAACCAAGAT 1887
Qy   394 GluIleSerGlnArg------AsnArgGlnLeuProSerAspGlyLysLysMetValHis 411
Db  1888 GAACTTGACCCCCAGTGTGTGGAAAGAAAGACCATCTCCCCAGGC---CGTGCCATCACC 1944
Qy   412 ValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThrProThrLeuGlnGlyLeu 431
Db  1945 ATACACAACGGCACCTTCTCCTGGTCCAAG---GACCTGCCTCCCACCCTTCACAGCMTA 2001
Qy   432 SerPheThrValArgProGlyGluLeuLeuAlaValValGlyProValGlyAlaGlyLys 451
Db  2002 AACATTCAAATCCCGAAGGGGGCATTGGTGGCTGTGGTGGGACCTGTGGGCTGTGGGAAG 2061
Qy   452 SerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHisGlyLeuValSerVal 471
Db  2062 TCTTCCCTGGTGTCTGCCTTGCTCGGAGAGATGGAGAAGCTGGAAGGTGCAGTGTCTGTA 2121
Qy   472 HisGlyArgIleAlaTyrValSerGlnGlnProTrpValPheSerGlyThrLeuArgSer 491
Db  2122 AAGGGCTCTGTGGCCTACGTGCCCCAGCAGGCGTGGATCCAGAAYTGCACACTTCAGGAA 2181

Qy   492 AsnIleLeuPheGlyLysLysTyrGluLysGluArgTyrGluLysValIleLysAlaCys 511
Db  2182 AATGTGCTATTTGGCCAACCCATGAACCCCAAGCGCTACCAACAGGCTCTGGAGACGTGT 2241
Qy   512 AlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThrValIleGlyAspArg 531
Db  2242 GCCCTGCTAGCTGACCTAGATGTGCTTCCTGGTGGGGACCAGACAGAGATTGGAGAGAAG 2301
Qy   532 GlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAlaValTyrGln 551
Db  2302 GGCATTAACCTATCTGGAGGCCAGCGACAACGGGTGAGTTTGGCCCGAGCTGTTTATAGT 2361
Qy   552 AspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGluValSerArg 571
Db  2362 GACGCCAACATTTTTTTGCTGGATGACCCACTGTCGGCTGTGGACTCTCACGTGGCTAAG 2421
Qy   572 HisLeuPheGluLeuCysIleCysGln------IleLeuHisGluLysIleThrIleLeu 589
Db  2422 CATATCTTCGACCAAGTGATTGGACCAGAAGGTGTGCTGGCAGGCAAGACTCGGGTGCTG 2481
Qy   590 ValThrHisGlnLeuGlnTyrLeuLysAlaAlaSerGlnIleLeuIleLeuLysAspGly 609
Db  2482 GTAACCCATGGCATCAGCTTCCTGCCCCAGACGGACTTTATCATTGTGCTTGCTGACGGA 2541
Qy   610 LysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIleAspPheGlySer 629
Db  2542 CAGATTACTGAGATGGGTCACTACTCCGAACTCCTGCAGCACGATGGCTCCTTTGCCAAC 2601
Qy   630 LeuLeuLysLys------------AspAsnGluGluSerGluGlnProProVal------ 643
Db  2602 TTCCTCCGAAACTATGCACCAGATGAAAACCAGGAGGCCAATGAAGGAGTCTTGCAACAT 2661
Qy   643 ------------------------------------------------------------ 643
Db  2662 GCAAATGAGGAGGTGCTCCTGCTTGAAGACACACTCAGCACCCACACAGACCTGACAGAC 2721
Qy   644 ------ProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSer 661
Db  2722 ACCGAGCCAGCCATATACGAGGTCCGCAAGCAGTTCATGAGAGAGATGAGCTCCTTGTCT 2781
Qy   662 GlnGln---------SerSerArgProSerLeuLys------AspGlyAlaLeuGluSer 676
Db  2782 TCTGAAGGAGAGGGCCAGAACCGGCCTGTGCTCAAGAGATATACGAGTTCACTGGAGAAG 2841
Qy   677 Gln------------AspThrGluAsnValProValThrLeuSerGluGluAsnArgSer 692
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Qy   733 TrpTrpLeuSerTyrTrpAlaAsnLysGlnSerMetLeuAsnValThrValAsnGlyGly 752
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Qy   753 GlyAsnValThrGluLysLeuAspLeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThr 772
Db  3064 CAGAACAACACC---------------TCCGTAAGGCTGGGAGTCTACGCCACCCTA--- 3105
Qy   773 ValAlaThrValLeuPheGlyIleAlaArgSerLeuLeuVal------------PheTyr 788
Db  3106 ------------------GGAATACTGCAAGGGCTCCTGGTCATGCTGTCGGCCTTCACC 3147
Qy   789 ValLeuValAsnSerSerGlnThr---------LeuHisAsnLysMetPheGluSerIle 805
Db  3148 ATGGTGGTTGGCGCTATCCAGGCTGCCCGCCTGCTGCACACAGCTCTGTTGCACAACCAG 3207
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Qy        806 LeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArgPhe 825
Db       3208 ATCCGTGCGCCTCARTCCTTCTTTGACACGACGCCCTCAGGCCGCATCCTCAATCGTTTC 3267

Qy        826 SerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGln 845
Db       3268 TCCAAGGACATATACGTCATCSATGAGGTTCTGGCCCCCACCATCCTCATGCTGTTCAAT 3327

Qy        846 ThrLeuLeuGlnValValGlyValValSerValAlaValAlaValIleProTrpIleAla 865
Db       3328 TCATTCTACACATCCATCTCCACCATTGTGGTCATCGTGGCCAGCACGCCACTCTTCTGC 3387

Qy        866 IleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrPheLeuGluThr 885
Db       3388 GTGGTTGTTCTTCCTCTGGCTGTGTTCTATGGCTTCGTGCAGCGCTTCTATGTGGCCACA 3447

Qy        886 SerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSerHisLeuSer 905
Db       3448 TCGAGGCAGCTGAAGAGACTGGAATCCGTTAGCCGCTCGCCCATCTTCTCCCACTTCTCG 3507

Qy        906 SerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGluGluArgCysGlnGlu 925
Db       3508 GAGACAGTAACTGGCACCAGTGTCATTCGGGCCTACGGCCGAGTCCAAGACTTCAAGGTC 3567

Qy        926 LeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeuPheLeuThrThrSer 945
Db       3568 CTCAGTGATGCTAAGGTGGATAGCAACCAGAAGACCACTTATCCTTACATCGCCTCCAAC 3627

Qy        946 ArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPhe 965
Db       3628 CGGTGGCTGGGTGTCCACGTGGAGTTTGTGGGGAACTGCGTGGTGCTCTTCTCCGCGCTG 3687

Qy        966 GlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyr 985
Db       3688 TTTGCAGTGATCGGGAGAAACAGCTTGAATCCAGGGCTTGTGGGTCTTTCCGTGTCCTAT 3747

Qy        986 AlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSerAlaGluValGluAsn 1005
Db       3748 GCCTTACAGGTGACCTTGAGTTTGAATTGGATGATACGGACGCTATCCGACCTGGAGTCT 3807

Qy       1006 MetMetIleSerValGluArgValIleGluTyrThrAspLeuGluLysGluAlaProTrp 1025
Db       3808 AATATCATAGCCGTGGAGAGAGTCAAGGAGTACTCTAAGACGGAGACTGAGGCTCCCTGG 3867

Qy       1026 GluTyrGln---LysArgProProProAlaTrpProHisGluGlyValIleIlePheAsp 1044
Db       3868 GTGTTGGAGAGCAACCGTGCTCCAGAAGGCTGGCCCAGGAGTGGGGTGGTAGAGTTCCGG 3927

Qy       1045 AsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHisLeuThrAlaLeu 1064
Db       3928 AACTATTCGGTGCGGTACCGCCCGGGCCTCGAGTTGGTGCTGAAGAATTTGACTCTGCAT 3987

Qy       1065 IleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeu 1084
Db       3988 GTGCAGGGTGGGGAGAAGGTAGGCATCGTGGGCCGCACTGGGGCTGGCAAATCTTCCATG 4047

Qy       1085 IleSerAlaLeuPheArgLeuSerGlu---ProGluGlyLysIleTrpIleAspLysIle 1103
Db       4048 ACTCTTTGCCTATTCCGAATCCTGGAGGCCGCAGAGGGTGAGATCTTCATTGACGGGCTC 4107

Qy       1104 LeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGlu 1123
Db       4108 AATGTGGCACACATTGGCCTCCATGACCTGCGTTCACAACTCACCATCATCCCTCAGGAC 4167

Qy       1124 ProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThrAsp 1143
Db       4168 CCCATCCTGTTCTCGGGCACGCTGCGCATGAACCTCGATCCCTTTGGCCGTTACTCGGAC 4227

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Db       4228 GAGGACATCTGGAGGACCCTGGAGCTATCCCACCTGAGTGCATTTGTGAGCAGCCAGCCG 4287

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Db       4288 ACAGGCCTGGATTTTCAGTGCTCTGAGGGTGGGGATAATCTCAGTGTTGGCCAGAGGCAG 4347

Qy       1184 LeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAla 1203
Db       4348 CTCGTGTGCCTAGCCCGAGCCCTGCTCCGAAAGAGCCGTGTCCTGGTTTTAGACGAGGCC 4407

Qy       1204 ThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPhe 1223
Db       4408 ACCGCTGCCATTGACCTGGAGACTGATGACCTCATCCAGGGTACCATCCGTACCCAGTTT 4467

Qy       1224 AlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLys 1243
Db       4468 GAAGACTGCACTGTACTGACCATCGCCCACCGGCTCAACACAATCATGGACTACAACCGG 4527

Qy       1244 IleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrValLeuLeuGln 1263-
Db       4528 GTCCTGGTCTTGGACAAAGGAGTAGTAGCTGAATTTGATTCTCCAGTAAACCTCATTGCA 4587

Qy       1264 AsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAla 1279
Db       4588 ---GCTGGAGGCATCTTCTATGGGATGGCCAAAGATGCAGGACTCGCC 4632
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Search completed: March 14, 2006, 16:34:37
Job time : 1959 secs